

GenCore version 5.1.4_p5_4578
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OM protein - nucleic search, using frame_plus_p2n model.

Run on: May 23, 2003, 05:34:57 ; Search time 2038 Seconds
 (Without alignments)
 628.324 Million cell updates/sec

Title: Perfect score: 197
 Sequence: 1 ANSFLXLRqqSLRXCCIXX..... XXAKXIFedVDDTLAFWSKH 44

Scoring table: BLOSUM62

| | | | |
|---------|------|---------|-----|
| Xgapext | 0.0 | Xgapext | 0.5 |
| Ygapext | 10.0 | Ygapext | 0.5 |
| Fgap | 6.0 | Fgapext | 7.0 |
| Delop | 6.0 | Delet | 7.0 |

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database : GenEmbl:*

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| 2: gb_htq:* | 11: gb_htq:* | 20: gb_htq:* | 29: gb_htq:* | 38: gb_htq:* |
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| 4: gb_ov:* | 13: gb_ov:* | 22: gb_ov:* | 31: gb_ov:* | 40: gb_ov:* |
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| 7: gb_ph:* | 16: gb_ph:* | 25: gb_ph:* | 34: gb_ph:* | 43: gb_ph:* |
| 8: gb_pl:* | 17: gb_pl:* | 26: gb_pl:* | 35: gb_pl:* | 44: gb_pl:* |
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| 17: em_hum:* | 26: em_hum:* | 35: em_hum:* | 44: em_hum:* | 53: em_hum:* |
| 18: em_in:* | 27: em_in:* | 36: em_in:* | 45: em_in:* | 54: em_in:* |
| 19: em_mu:* | 28: em_mu:* | 37: em_mu:* | 46: em_mu:* | 55: em_mu:* |
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| 22: em_ov:* | 31: em_ov:* | 40: em_ov:* | 49: em_ov:* | 58: em_ov:* |
| 23: em_pat:* | 32: em_pat:* | 41: em_pat:* | 50: em_pat:* | 59: em_pat:* |
| 24: em_ph:* | 33: em_ph:* | 42: em_ph:* | 51: em_ph:* | 60: em_ph:* |
| 25: em_pl:* | 34: em_pl:* | 43: em_pl:* | 52: em_pl:* | 61: em_pl:* |
| 26: em_ro:* | 35: em_ro:* | 44: em_ro:* | 53: em_ro:* | 62: em_ro:* |
| 27: em_sts:* | 36: em_sts:* | 45: em_sts:* | 54: em_sts:* | 63: em_sts:* |
| 28: em_un:* | 37: em_un:* | 46: em_un:* | 55: em_un:* | 64: em_un:* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | | | | | |
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| Result No. | Score | Query Match | Length | DB ID | Description |
| 1 | 179 | 90.9 | 1386 | 6 AX207787 | AX207787 Sequence |
| 2 | 179 | 90.9 | 1386 | 6 AX207788 | AX207788 Sequence |
| 3 | 174 | 88.3 | 1386 | 6 AX207785 | AX207785 Sequence |
| 4 | 174 | 88.3 | 1386 | 6 AX207786 | AX207786 Sequence |
| 5 | 174 | 88.3 | 1386 | 6 AX212332 | AX212332 Sequence |
| 6 | 174 | 88.3 | 1386 | 6 AX212333 | AX212333 Sequence |
| 7 | 168 | 85.3 | 1386 | 6 AX149846 | AX149846 Sequence |
| 8 | 167 | 84.8 | 1386 | 6 AX149845 | AX149845 Sequence |
| 9 | 167 | 84.8 | 1386 | 6 AX212334 | AX212334 Sequence |
| 10 | 162 | 81.2 | 1386 | 6 AX149844 | AX149844 Sequence |
| 11 | 160 | 81.2 | 1257 | 6 AX42736 | AX42736 Sequence |
| 12 | 160 | 81.2 | 1260 | 6 AX044041 | AX044041 Sequence |
| 13 | 160 | 81.2 | 1260 | 6 AX149839 | AX149839 Sequence |
| 14 | 160 | 81.2 | 1260 | 6 AX207783 | AX207783 Sequence |
| 15 | 160 | 81.2 | 1260 | 6 AX212330 | AX212330 Sequence |
| 16 | 160 | 81.2 | 1260 | 6 AX0579 | 10579 Sequence 1 |
| 17 | 160 | 81.2 | 1383 | 6 AX42734 | AX42734 Sequence |
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| 22 | 160 | 81.2 | 1386 | 6 AX044045 | AX044045 Sequence |
| 23 | 160 | 81.2 | 1386 | 6 AX149840 | AX149840 Sequence |
| 24 | 160 | 81.2 | 1386 | 6 AX207784 | AX207784 Sequence |
| 25 | 160 | 81.2 | 1386 | 6 AX212331 | AX212331 Sequence |
| 26 | 160 | 81.2 | 1386 | 6 E01708 | E01708 DNA sequence |
| 27 | 160 | 81.2 | 1386 | 6 E016643 | 106643 Sequence 1 |
| 28 | 160 | 81.2 | 1386 | 6 E018112 | 108112 Sequence 1 |
| 29 | 160 | 81.2 | 1389 | 6 E02492 | E02492 DNA encod1 |
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| 31 | 160 | 81.2 | 1792 | 9 BC034377 | Homo sapi |
| 32 | 160 | 81.2 | 1843 | 6 AX411026 | AX411026 Sequence |
| 33 | 160 | 81.2 | 1843 | 9 HSPr0C | X02750 Human Liver |
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| 35 | 156 | 79.2 | 1386 | 6 AX149842 | AX149842 Sequence |
| 36 | 156 | 79.2 | 1759 | 6 E0189 | E0189 DNA encod1 |
| 37 | 155 | 78.7 | 1260 | 6 E00961 | E00961 cDNA encod1 |
| 38 | 155 | 78.7 | 1386 | 6 AX149641 | AX149641 Sequence |
| 39 | 157 | 71.1 | 1499 | 9 MUSC1 | D1045 Mouse mRNA |
| 40 | 140 | 71.1 | 1603 | 10 BC013896 | BC013896 Mus muscu |
| 41 | 139 | 70.6 | 1543 | 6 AX401899 | AX401899 Sequence |
| 42 | 139 | 70.6 | 1543 | 6 RNPR0C | X65336 R norvegicu |
| 43 | 138 | 70.1 | 1558 | 4 OC04933 | U49933 Oryctolagus |
| 44 | 135 | 68.5 | 271 | 6 E02245 | E02245 DNA sequenc |
| 45 | 1383 | 68.5 | 6 E02246 | E02246 DNA sequenc | |

ALIGNMENTS

AX207787 AX207787 1386 bp DNA linear PAT 31-AUG-2001
 DEFINITION Sequence 11 from Patent WO0157193.
 ACCESSION AX207787
 VERSION AX207787.1 GI:15422463
 KEYWORDS SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1386)
 AUTHORS Gerlitz, B. E. and Jones, B. E.
 TITLE Protein c derivatives
 JOURNAL Patent: WO 0157193 A 11 09-AUG-2001;
 ELI LILLY AND COMPANY (US)
 FEATURES source
 /organism="Homo sapiens"
 BASE COUNT 286 a 416 c 443 g 241 t
 ORIGIN

Alignment Scores:
 Pred. No.: 6. 35e-24 Length: 1386
 Score: 179.00 Matches: 35
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 Best Local Similarity: 79.55% Mismatches: 9
 Query Match: 90.86% Indels: 0
 DB: 6 Gaps: 0

SEQ1-4EDITS (1-44) x AX207787 (1-1386)

Qy 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***CysIle***** 20
 Db 127 GCAACACCTTCTGGAGGACCTCCCTCAGGGAGCTGGAGGGAGTCATAGGGAG 186
 REFERENCE 1 (bases 1 to 1385)
 AUTHORS Gerlitz, B. E. and Jones, B. E.
 TITLE Protein c derivatives
 JOURNAL Patent: WO 0157193 A 9 09-Aug-2001;
 ELI LILLY AND COMPANY (US)
 FEATURES source
 /organism="Homo sapiens"
 BASE COUNT 285 a 417 c 443 g 241 t
 ORIGIN

RESULT 2

AX207788 AX207788 1386 bp DNA linear PAT 31-AUG-2001
 DEFINITION Sequence 12 from Patent WO0157193.
 ACCESSION AX207788
 VERSION AX207788.1 GI:15422464
 KEYWORDS SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1386)
 AUTHORS Gerlitz, B. E. and Jones, B. E.
 TITLE Protein c derivatives
 JOURNAL Patent: WO 0157193 A 12 09-AUG-2001;
 ELI LILLY AND COMPANY (US)
 FEATURES source
 /organism="Homo sapiens"
 BASE COUNT 286 a 415 c 444 g 241 t
 ORIGIN

Alignment Scores:
 Pred. No.: 6. 35e-24 Length: 1386
 Score: 179.00 Matches: 35
 Percent Similarity: 79.55% Conservative: 0
 Best Local Similarity: 79.55% Mismatches: 9
 Query Match: 90.86% Indels: 0

RESULT 3

AX207785 AX207785 1386 bp DNA linear PAT 31-AUG-2001
 DEFINITION Sequence 9 from Patent WO0157193.
 ACCESSION AX207785
 VERSION AX207785.1 GI:15422461
 KEYWORDS SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1385)
 AUTHORS Gerlitz, B. E. and Jones, B. E.
 TITLE Protein c derivatives
 JOURNAL Patent: WO 0157193 A 9 09-Aug-2001;
 ELI LILLY AND COMPANY (US)
 FEATURES source
 /organism="Homo sapiens"
 BASE COUNT 285 a 417 c 443 g 241 t
 ORIGIN

Alignment Scores:
 Pred. No.: 5. 61e-23 Length: 1386
 Score: 174.00 Matches: 34
 Percent Similarity: 77.27% Conservative: 0
 Best Local Similarity: 77.27% Mismatches: 10
 Query Match: 80.32% Indels: 0
 DB: 6 Gaps: 0

SEQ1-4EDITS (1-44) x AX207785 (1-1386)

Qy 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***CysIle***** 20
 Db 127 GCAACACTCTCTGGAGGACCTCCCTCAGGGAGCTGGAGGGAGTCATAGGGAG 186
 REFERENCE 1 (bases 1 to 1385)
 AUTHORS Gerlitz, B. E. and Jones, B. E.
 TITLE Protein c derivatives
 JOURNAL Patent: WO 0157193 A 9 09-Aug-2001;
 ELI LILLY AND COMPANY (US)
 FEATURES source
 /organism="Homo sapiens"
 BASE COUNT 285 a 417 c 443 g 241 t
 ORIGIN

RESULT 4

AX207786 AX207786 1386 bp DNA linear PAT 31-AUG-2001
 DEFINITION Sequence 10 from Patent WO0157193.
 ACCESSION AX207786
 VERSION AX207786.1 GI:15422462
 KEYWORDS SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1386)

AUTHORS Gerlitz, B.E. and Jones, B.E.
 PROTEIN C derivatives
 JOURNAL
 PATENT WO 0157193-A 10-09-AUG-2001;
 ELI LILLY AND COMPANY (US)
 Location/Qualifiers

FEATURES SOURCE
 1. .1386
 /organism="Homo sapiens"
 /db-xref="taxon:9606"
 BASE COUNT 285 a 416 c 444 g 241 t
 ORIGIN

Alignment Scores:
 Pred. NO.: 5.61e-23
 Score: 174.00
 Percent Similarity: 77.27%
 Best Local Similarity: 87.27%
 Query Match: 6

SEQ1-4EDITS (1-44) x AX207786 (1-1386)

QY 1 AlaAsnSerPheLeu*****LeuArgGlySerLeu***Arg***CysIle***** 20
 Db 127 GCCAACTCCCTCTGAGGAGCTCGTCACGGGACCTGAGCGAGTCATGGAGG 186

QY 21 IleCysAspHe*****AlaLys***IlePheGluAspValAspAspThrLeuAlaPhe 40
 Db 187 ATCTGTGACTTCGAGGAGGCCAAGGAATTTCGAAGATGGATGACACACTGGCCTTC 246

QY 41 TrpSerLySHis 44
 Db 247 TGGTCCAAGCAC 258

RESULT 5
 Locus AX212332
 Definition Sequence 8 from Patent WO159084.
 Accession AX212332.1
 Version GI:15524088
 Keywords
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 (bases 1 to 1386)
 Gerlitz, B.E., Grinnell, B.W. and Jones, B.E.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PATENT WO 0159084-A 9 16-AUG-2001;
 ELI LILLY AND COMPANY (US)
 Location/Qualifiers

1. .1386

FEATURES SOURCE
 /organism="Homo sapiens"
 /db-xref="taxon:9606"
 BASE COUNT 285 a 417 c 443 g 241 t
 ORIGIN

Alignment Scores:
 Pred. NO.: 5.61e-23
 Score: 174.00
 Percent Similarity: 77.27%
 Best Local Similarity: 87.27%
 Query Match: 6

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QY 1 AlaAsnSerPheLeu*****LeuArgGlySerLeu***Arg***CysIle***** 20
 Db 127 GCCAACTCCCTCTGAGGAGCTCGTCACGGGACCTGAGCGAGTCATGGAGG 186

QY 21 IleCysAspHe*****AlaLys***IlePheGluAspValAspAspThrLeuAlaPhe 40
 Db 187 ATCTGTGACTTCGAGGAGGCCAAGGAATTTCGAAGATGGATGACACACTGGCCTTC 246

QY 41 TrpSerLySHis 44
 Db 247 TGGTCCAAGCAC 258

RESULT 6
 Locus AX212333
 Definition Sequence 9 from Patent WO159084.
 Accession AX212333.1
 Version GI:15524089
 Keywords
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Gerlitz, B.E., Grinnell, B.W. and Jones, B.E.
 Protein C derivatives
 Patent: WO 0159084-A 9 16-AUG-2001;
 ELI LILLY AND COMPANY (US)
 Location/Qualifiers

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FEATURES SOURCE
 /organism="Homo sapiens"
 /db-xref="taxon:9606"
 BASE COUNT 285 a 418 c 442 g 241 t
 ORIGIN

Alignment Scores:
 Pred. NO.: 5.61e-23
 Score: 174.00
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 Best Local Similarity: 88.32%
 Query Match: 6

SEQ1-4EDITS (1-44) x AX212333 (1-1386)

QY 1 AlaAsnSerPheLeu*****LeuArgGlySerLeu***Arg***CysIle***** 20
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QY 21 IleCysAspHe*****AlaLys***IlePheGluAspValAspAspThrLeuAlaPhe 40
 Db 187 ATCTGTGACTTCGAGGAGGCCAAGGAATTTCGAAGATGGATGACACACTGGCCTTC 246

QY 41 TrpSerLySHis 44
 Db 247 TGGTCCAAGCAC 258

RESULT 7
 Locus AX149646
 Definition Sequence 16 from Patent WO0136462.
 Accession AX149646.1
 Version GI:14348045
 Keywords
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 (bases 1 to 1386)
 Gerlitz, B.E., Grinnell, B.W., Huang, L. and Jones, B.E.
 Protein C derivatives
 Patent: WO 0136462-A 16 25-MAY-2001;
 ELI LILLY AND COMPANY (US)
 Location/Qualifiers

1. .1386

FEATURES SOURCE
 /organism="Homo sapiens"
 /db-xref="taxon:9606"
 BASE COUNT 288 a 416 c 442 g 240 t
 ORIGIN

QY 1 AlaAsnSerPheLeu*****LeuArgGlySerLeu***Arg***CysIle***** 20
 Db 127 GCCAACTCCCTCTGAGGAGCTCGTCACGGGACCTGAGCGAGTCATGGAGG 186

QY 21 IleCysAspHe*****AlaLys***IlePheGluAspValAspAspThrLeuAlaPhe 40
 Db 187 ATCTGTGACTTCGAGGAGGCCAAGGAATTTCGAAGATGGATGACACACTGGCCTTC 246

Alignment Scores: 7.67e-22
 Pred. No.: 168.00
 Score: 79.55%
 Percent Similarity: 72.73%
 Best Local Similarity: 85.28%
 Query Match: 6
 DB: SEQ1-4EDITS (1-44) x AX149646 (1-1386)

QY 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***CysIle***** 20
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 QY 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspPheLeuAlaPhe 40
 Db 187 ATCTGTGACTTCGAGGAGCCAGGAATTTCACAAATGTCATGACACTGCGCTC 246

QY 41 TrpSerIlyHis 44
 Db 247 TGGTCCAAGCAC 258

RESULT 8
 LOCUS AX149645
 DEFINITION Sequence 15 from Patent WO0136462.
 ACCESSION AX149645
 VERSION 1.1
 SOURCE human
 KEYWORDS
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1386)
 AUTHORS Gerlitz, B. E., Grinnell, B. W., Huang, L. and Jones, B. E.
 TITLE Protein c derivatives
 JOURNAL Patent: WO 0136462-A 15 25-MAY-2001;
 ELI LILLY AND COMPANY (US)
 FEATURES
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 288 a
 ORIGIN 416 c 442 g 240 t

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 Query Match: 6
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SEQ1-4EDITS (1-44) x AX149645 (1-1386)

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 QY 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspPheLeuAlaPhe 40
 Db 187 ATCTGTGACTTCGAGGAGCCAGGAATTTCACAAATGTCATGACACTGCGCTC 246

QY 41 TrpSerIlyHis 44
 Db 247 TGGTCCAAGCAC 258

RESULT 10
 LOCUS AX149644
 DEFINITION Sequence 14 from Patent WO0136462.
 ACCESSION AX149644
 VERSION 1.1
 SOURCE human
 KEYWORDS
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1386)
 AUTHORS Gerlitz, B. E., Grinnell, B. W., Huang, L. and Jones, B. E.
 TITLE Protein c derivatives
 JOURNAL Patent: WO 0136462-A 14 25-MAY-2001;
 ELI LILLY AND COMPANY (US)
 FEATURES
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 288 a
 ORIGIN 417 c 441 g 240 t

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 QY 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspPheLeuAlaPhe 40
 Db 187 ATCTGTGACTTCGAGGAGCCAGGAATTTCACAAATGTCATGACACTGCGCTC 246

QY 41 TrpSerIlyHis 44
 Db 247 TGGTCCAAGCAC 258

RESULT 9
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 DEFINITION Sequence 10 from Patent WO0159084.
 ACCESSION AX212334
 VERSION AX212334.1 GI:15524090

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SEQ1-4EDITS (1-44) x AX149644 (1-1386)

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 QY 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspPheLeuAlaPhe 40
 Db 187 ATCTGTGACTTCGAGGAGCCAGGAATTTCACAAATGTCATGACACTGCGCTC 246

QY 41 TrpSerIlyHis 44
 Db 247 TGGTCCAAGCAC 258

RESULT 9
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 DEFINITION Sequence 10 from Patent WO0159084.
 ACCESSION AX212334
 VERSION AX212334.1 GI:15524090

ACCESION AX044041
VERSION AX044041.1 GI:11342920
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1260)
AUTHORS Gerlitz, B. E. and Jones, B. E.
TITLE Protein c derivatives
JOURNAL Patent: WO 0066734-A 6 09-NOV-2000;
ELI LILLY AND COMPANY (US)
Location/Qualifiers 1. .1260
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/db_xref="taxon:9606"
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BASE COUNT 265 a 375 c 407 g 213 t
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Db 1 GCCAACTCCCTCGAGGAGCTCGTCACAGCAGCCCTGGAGGAGTCATAGGGAG 60
Qy 21 IleCysAspHe*****AlaLys***IlePheGluAspValAspAspThrLeuAlaPhe 40
Db 61 ATCTGAGCTCGAGGCCAAAGGAAATTCCAAATGTTGAGACACACTGGCTTC 120
RESULT 13
LOCUS AX149639 1260 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 9 from Patent WO0136462.
ACCESSION AX149639
VERSION AX149639.1 GI:14348038
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1260)
AUTHORS Gerlitz, B. E., Grinnell, B. W., Huang, L. and Jones, B. E.
TITLE Protein c derivatives
JOURNAL Patent: WO 0136462-A 9 25-MAY-2001;
ELI LILLY AND COMPANY (US)
Location/Qualifiers 1. .1260
/organism="Homo sapiens"
/db_xref="taxon:9606"
FEATURES source
BASE COUNT 265 a 375 c 407 g 213 t
ORIGIN
Alignment Scores: 2.26e-20 Length: 1260
Pred. No.: 160.00 Matches: 31
Score: 75.00% Conservative: 2
Percent Similarity: 70.45% Mismatches: 11
Best Local Similarity: 81.22% Indels: 0
Query Match: 6 Gaps: 0
SEQ1-4EDITS (1-44) x AX044041 (1-1260)
Qy 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu**Arg***CysIle***** 20
Db 1 GCCAACTCCCTCGAGGAGCTCGTCACAGCAGCCCTGGAGGAGTCATAGGGAG 60
Qy 21 IleCysAspHe*****AlaLys***IlePheGluAspValAspAspThrLeuAlaPhe 40
Db 61 ATCTGAGCTCGAGGCCAAAGGAAATTCCAAATGTTGAGACACACTGGCTTC 120
RESULT 12
LOCUS AX044041 1260 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 6 from Patent WO0066754.
BASE COUNT 265 a 375 c 407 g 213 t
ORIGIN
Alignment Scores: 2.26e-20 Length: 1260
Pred. No.: 160.00 Matches: 31
Score: 75.00% Conservative: 2
Percent Similarity: 70.45% Mismatches: 11
Best Local Similarity: 81.22% Indels: 0
Query Match: 6 Gaps: 0
SEQ1-4EDITS (1-44) x AX149639 (1-1260)

GenCore version 5.1.4_p5_4578
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On protein - nucleic search, using frame_plus_p2n model

Run on: May 23, 2003, 04:55:39 ; Search time 211 Seconds
(without alignments)
411.153 Million cell updates/sec

SEQ1-4EDITS

Title: Perfect score:
Sequence: 1 ANSFLXXLRLqgSLXRXCTXX.....XXAKKXIRDvDDTLAFWSKH 44

Scoring table: BL0SUM62

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Ygapext 10.0 , Ygapext 0.5
Egapext 6.0 , Egapext 7.0
Delop 6.0 , Delext 7.0

Searched: 218239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITSBITS -START=1 -END=1 -MATRIX=biolum62 -TRANS=human10.cds
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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| 2 | 179 | 90.9 | 1386 | 22 | ADD15228 |
| 3 | 179 | 90.9 | 1386 | 22 | AHH26355 |
| 4 | 179 | 90.9 | 1386 | 22 | AHH26356 |
| 5 | 174 | 88.3 | 1386 | 22 | ADD15225 |
| 6 | 174 | 88.3 | 1386 | 22 | AAD15226 |
| 7 | 174 | 88.3 | 1386 | 22 | AHH26353 |
| 8 | 174 | 88.3 | 1386 | 22 | AHH26354 |
| 9 | 160 | 81.2 | 1245 | 21 | AZ246750 |
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| 11 | 160 | 81.2 | 1260 | 7 | AAN60001 |
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| 16 | 160 | 81.2 | 1386 | 9 | AAB81403 |
| 17 | 160 | 81.2 | 1386 | 10 | AAN90024 |
| 18 | 160 | 81.2 | 1386 | 10 | AAN90187 |
| 19 | 160 | 81.2 | 1386 | 18 | AAT79724 |
| 20 | 160 | 81.2 | 1386 | 22 | AAD15224 |
| 21 | 160 | 81.2 | 1386 | 22 | AHH26352 |
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| 23 | 160 | 81.2 | 1386 | 22 | AAC83313 |
| 24 | 160 | 81.2 | 1386 | 22 | AAC83314 |
| 25 | 160 | 81.2 | 1386 | 22 | AAC83315 |
| 26 | 160 | 81.2 | 1389 | 11 | AHQ03218 |
| 27 | 160 | 81.2 | 1685 | 15 | AHQ72994 |
| 28 | 160 | 81.2 | 1754 | 12 | AHQ13357 |
| 29 | 160 | 81.2 | 1754 | 12 | AHQ13357 |
| 30 | 160 | 81.2 | 1755 | 12 | AHQ12678 |
| 31 | 160 | 81.2 | 1755 | 17 | AAT32795 |
| 32 | 160 | 81.2 | 1756 | 9 | AAB81563 |
| 33 | 160 | 81.2 | 1843 | 22 | AAP54035 |
| 34 | 160 | 81.2 | 1843 | 22 | AAP54050 |
| 35 | 160 | 81.2 | 1843 | 24 | ABN9175 |
| 36 | 139 | 70.6 | 1543 | 24 | AHQ3668 |
| 37 | 135 | 68.5 | 1383 | 11 | AAC01764 |
| 38 | 119 | 60.4 | 11715 | 9 | ANB1564 |
| 39 | 119 | 60.4 | 11724 | 8 | AAN10102 |
| 40 | 119 | 60.4 | 11724 | 22 | AHH57497 |
| 41 | 119 | 60.4 | 11725 | 17 | AAT32796 |
| 42 | 119 | 60.4 | 11725 | 18 | AAT79723 |
| 43 | 119 | 60.4 | 11725 | 20 | AAZ32179 |
| 44 | 119 | 60.4 | 11725 | 22 | AAF54051 |
| 45 | 116 | 58.9 | 271 | 10 | AAN93748 |

ALIGNMENTS

RESULT 1

ID AAD15227 standard: DNA: 1386 BP.

XX AAD15227:

XX 01-NOV-2001 (first entry)

DE Human protein C derivative encoding DNA #3.

XX Human; protein C derivative; anticoagulation activity; thrombosis; serpin inactivation; acute coronary syndrome; myocardial infarction; vascular occlusive disorder; hypercoagulable state; angina; sepsis; disseminated intravascular coagulation; DIC; burn; transplantation; sickle cell disease; viral haemorrhagic fever; protein C deficiency; haemolytic uremic syndrome; acute arterial thrombosis; protein C deficiency; thromboembolism; prothrombotic disorder; gene therapy; thalassemia; ds.

Pred. No.: 1.36e-23 **Length:** 1386
Score: 179.00 **Matches:** 35
Percent Similarity: 79.55% **Conservative:** 0
Best Local Similarity: 79.55% **Mismatches:** 9
Query Match: 22 **Indels:** 0
DB: 22 **Gaps:** 0

SEQ1-4EDITS (1-44) x AAD15228 (1-1386)
Qy 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***Cyste***** 20
Db 127 GCCAACTCTTCTGGAGGAGCCTGGCTAGGGAGCCGAGTGCAATAGAGGAG 186
Qy 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspAspThrLeuAlaPhe 40
Db 187 ATCTGTGACTTCCAGGAGGCCAAGGAATTTCCAGATGTGGATGACACTGGCCATC 246
Qy 41 TrpSerLysHis 44
Db 247 TGGTCCAAGCAC 258

RESULT 3
AAH26365
ID AAH26365 standard; cDNA; 1386 BP.
XX
AC AAH26365;
XX
DT 15-OCT-2001 (first entry)
XX
DE DNA encoding human protein C derivative.
XX
KW Protein C; human; coronary syndrome; thrombosis; angina;
KW myocardial infarction; vascular occlusive disorder;
KW hypercoagulation; sepsis; protein C deficiency; occlusion;
KW thromboembolism; stenosis; antibacterial; immunosuppressive;
KW thrombolytic; cardiant; antiangiinal; anticoagulant; gene therapy;
KW mutant; ss.
OS Homo sapiens.
Synthetic.
XX
FH Key
PT sig_peptide
FT /*tag= a
FT mat_peptide
FT /*tag= b
FT /note= "encodes AAB82677"
XX
PN WO20015193-A2.
XX
PD 09-AUG-2001.
XX
PF 19-JAN-2001; 2001WO-US0020.
XX
PR 02-FEB-2000; 2000US-0179801.
PR 14-MAR-2000; 2000US-0189197.
XX
PA (ELIL) LILLY & CO ELI.
PI Gerlitz BE, Jones BE;
XX
DR WPI: 2001496919/54.
DR P-PSDB; AAB82677.
XX
PT Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute arterial thrombotic occlusion, and thromboembolism.
PT Disclosure: page 60-61; 63pp; English.
XX
CC The present sequence is that of DNA encoding a claimed human protein C derivative (see AAB82677), in which His at position 10 of the mature wild-type protein C sequence is substituted with Gln, Ser at

CC position 11 with Gly, Gln at position 32 with Glu, Asn at position 33 with Asp and Leu at position 194 with Ser. The invention relates to protein C derivatives having at least 2 amino acid substitutions, and to recombinant DNA molecules encoding such derivatives. These derivatives have increased anticoagulant activity and resistance to inactivation by serpins compared with wild-type human protein C but retain the biological activity of the wild-type protein. Recombinant DNA molecules encoding preferred protein C derivatives are given in AAB26365-66. Also claimed are a vector comprising the recombinant DNA, transformed host cells and a method of producing the human protein C derivative. The protein C derivatives are useful for treating coronary syndromes and disease states predisposing to thrombosis (e.g., myocardial infarction and unstable angina), vascular occlusive disorders and hypercoagulable states, sepsis (in combination with bactericidal permeability increasing protein or with tissue factor pathway inhibitor), thrombotic disorders (in combination with an anti-platelet agent or by local delivery through an intracoronary catheter), protein C deficiency, acute arterial thrombotic occlusion, thromboembolism, or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts. Human patients with genetically predisposed prothrombotic disorders may be treated by gene therapy (all claimed).

XX
SQ Sequence 1386 BP; 286 A; 416 C; 443 G; 241 T; 0 other;

Alignment Scores:
Pred. No.: 1.36e-23 **Length:** 1386
Score: 179.00 **Matches:** 35
Percent Similarity: 79.55% **Conservative:** 0
Best Local Similarity: 79.55% **Mismatches:** 9
Query Match: 90.86% **Indels:** 0
DB: 22 **Gaps:** 0

SEQ1-4EDITS (1-44) x AAH26365 (1-1386)
Qy 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***Cyste***** 20
Db 127 GCCAACTCTTCTGGAGGAGCCTGGCTAGGGAGCCGAGTGCAATAGAGGAG 186
Qy 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspAspThrLeuAlaPhe 40
Db 187 ATCTGTGACTTCCAGGAGGCCAAGGAATTTCCAGATGTGGATGACACTGGCCATC 246
Qy 41 TrpSerLysHis 44
Db 247 TGGTCCAAGCAC 258

RESULT 4
AAH26366
ID AAH26366 standard; cDNA; 1386 BP.
XX
AC AAH26366;
XX
DT 15-OCT-2001 (first entry)
XX
DE DNA encoding human protein C derivative.
XX
KW Protein C; human; coronary syndrome; thrombosis; angina;
KW myocardial infarction; vascular occlusive disorder;
KW hypercoagulation; sepsis; protein C deficiency; occlusion;
KW thromboembolism; stenosis; antibacterial; immunosuppressive;
KW thrombolytic; cardiant; antiangiinal; anticoagulant; gene therapy;
KW mutant; ss.
OS Homo sapiens.
Synthetic.
XX
FH Key
PT sig_peptide
FT 1..126
FT /*tag= a
FT mat_peptide
FT /*tag= b
FT /note= "encodes AAB82678"

Percent Similarity: 77.27% Conservative: 0
 Best Local Similarity: 77.27% Mismatches: 10
 Query Match: 88.32% Indels: 0
 DB: 0 Gaps: 0

SEQ1-4 EDITS (1-44) x AAD15225 (1-1386)

QY 1 AlaAsnSerPheLeu*****LeuArgGlySerLeu***Arg***CysIle***** 20
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 127 GCCAACTCTCCGAGGAGCTCCGTCAGGGAGGCCCTGGAGGAGCTGAGAGGAG 186
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspSerPheLeuAlaPhe 40
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 187 ATCTGTGACTCGAGGAGGCCAAGGAATTTCGAAGATGGATGACACACTGGCCTC 246
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 41 TrpSerLysIle 44
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 247 TGGTCCAAGGCAC 258

RESULT 6

AD15226 standard; DNA; 1386 BP.

XX

AC AAD15226;

XX

DT 01-NOV-2001 (first entry)

XX

DE Human protein C derivative encoding DNA #2.

XX

KW Human; protein C derivative; anticoagulation activity; thrombosis; serpin inactivation; acute coronary syndrome; myocardial infarction; vascular occlusive disorder; hypercoagulable state; angina; sepsis; disseminated intravascular coagulation; DIC; burn; transplantation; sickle cell disease; viral haemorrhagic fever; protein C deficiency; haemolytic uraemic syndrome; acute arterial thrombotic occlusion; thromboembolism; prothrombotic disorder; gene therapy; thalassaemia; ds. OS

XX

OS Homo sapiens.

XX

FT Key 127.1386

FT /tag= a

FT /product= "Human protein C derivative"

XX

PN WO20015084-A1.

XX

PD 16-AUG-2001.

XX

PP 02-FEB-2001; 2001WO-US01221.

XX

PR 11-FEB-2000; 2000US-0181948.

PR 14-MAR-2000; 2000US-0189199.

PA (ELIL) LILLY & CO ELL.

XX

PT Gerlitz BE, Grinnell BW, Jones BE;

XX

DR WPI; 2001-514662/56.

DR P-PSDB; AAE08428.

XX

PT Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions -

PS Disclosure; Page 53-54; 59pp; English.

XX

CC The invention relates to human protein C derivatives and nucleic acid molecules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and increased sensitivity to thrombin activation compared to wild type protein C, and retains the biological activity of the wild type human protein C. Protein C derivatives are useful in the manufacture of a medicament for the treatment of acute coronary syndromes e.g. myocardial infarction and unstable angina; and disease states predisposing to thrombosis; vascular occlusive disorders and hypercoagulable states e.g. disseminated intravascular coagulation (DIC), burns, transplants, thalassaemia, sickle cell disease, viral haemorrhagic fever and haemolytic uraemic syndrome; sepsis in combination with bacterial permeability increasing protein; thrombotic disorders in combination with an anti-platelet agent; protein C deficiency; acute arterial thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts in combination with a thrombolytic agent. Nucleic acid molecules of the invention are useful for treating humans with genetically predisposed prothrombotic disorders by gene therapy. The present sequence is human protein C derivative encoding DNA.

XX

Sequence 1386 BP; 285 A; 417 C; 443 G; 241 T; 0 other;

Alignment Scores:

Pred. No.: 1.198-22 Length: 1386
 Score: 174.00 Matches: 34
 Percent Similarity: 77.27% Conservative: 0
 Query Match: 88.32% Mismatches: 10
 DB: 22 Indels: 0
 AC Gaps: 0

SEQ1-4 EDITS (1-44) x AAD15225 (1-1386)

QY 1 AlaAsnSerPheLeu*****LeuArgGlySerLeu***Arg***CysIle***** 20
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 127 GCCAACTCTCCGAGGAGCTCCGTCAGGGAGGCCCTGGAGGAGCTGAGAGGAG 186
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspSerPheLeuAlaPhe 40
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 187 ATCTGTGACTCGAGGAGGCCAAGGAATTTCGAAGATGGATGACACACTGGCCTC 246
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 41 TrpSerLysIle 44
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 247 TGGTCCAAGGCAC 258

RESULT 7

AAH26363 standard; cDNA; 1386 BP.

XX

AC AAH26363;

XX

DT 15-OCT-2001 (first entry)

XX

DE DNA encoding human protein C derivative.

XX

PP Protein C; human; coronary syndrome; thrombosis; angina; myocardial infarction; vascular occlusive disorder; hypercoagulation; thromboembolism; stenosis; antibacterial; immunosuppressive; thrombolytic; cardiotonic; antianginal; anticoagulant; gene therapy; mutant; ss.

XX

OS Homo sapiens.

OS Synthetic.

XX

FT Key 1.126

FT sig-peptide /*tag= a

FT mat_peptide 127.1383

FT /*tag= b

FT /note= "encodes AAB82675"

XX

PN WO2001517193-A2.

XX

PD 09-AUG-2001.

XX

PR 19-JAN-2001; 2001WO-US00020.

PR 02-FEB-2000; 2000US-017801.

PR 14-MAR-2000; 2000US-0189197.

| | | | | | |
|--|------------------------|---|---------------|---------------|------|
| PA | XX | protein C; human; coronary syndrome; thrombosis; angina; | | | |
| PT | KW | myocardial infarction; vascular occlusive disorder; | | | |
| Gerlitz BE, Jones BE; | KW | hypercoagulation; sepsis; protein C deficiency; occlusion; | | | |
| XX | KW | thromboembolism; stenosis; antibacterial; immunosuppressive; | | | |
| DR | KW | thrombolytic; cardiot; antianginal; anticoagulant; gene therapy; | | | |
| XX | KW | mutant; ss. | | | |
| PR | XX | Novel human protein C derivative for treating, e.g., myocardial | | | |
| infarction, unstable angina, sepsis, thrombotic disorders, acute | XX | arterial thrombotic occlusion, and thromboembolism - | | | |
| PR | XX | Disclosure; Page 58-59; 63pp; English. | | | |
| PS | XX | The present sequence is that of DNA encoding a claimed human | | | |
| | CC | protein C derivative (see AAB82675), in which Ser at position 11 of | | | |
| | CC | the mature wild-type protein C sequence is substituted with Gly, Gln | | | |
| | CC | Gln at position 32 with Glu, Asn at position 33 with Asp, and Leu | | | |
| | CC | at position 194 with Ser. The invention relates to protein C | | | |
| | CC | derivatives having at least 2 amino acid substitutions, and to | | | |
| | CC | recombinant DNA molecules encoding such derivatives. These | | | |
| | CC | derivatives have increased anticoagulant activity and resistance to | | | |
| | CC | inactivation by serpins compared with wild-type human protein C but | | | |
| | CC | retain the biological activity of the wild-type protein. Recombinant | | | |
| | CC | DNA molecules encoding preferred protein C derivatives are given in | | | |
| | CC | AAH26363-66. Also claimed are a vector comprising the recombinant | | | |
| | CC | DNA, transformed host cells and a method of producing the human | | | |
| | CC | protein C derivative. The protein C derivatives are useful for | | | |
| | CC | treating coronary syndromes and disease states predisposing to | | | |
| | CC | thrombosis (e.g. myocardial infarction and unstable angina), | | | |
| | CC | vascular occlusive disorders and hypercoagulable states, sepsis (in | | | |
| | CC | combination with bactericidal permeability increasing protein or | | | |
| | CC | with tissue factor pathway inhibitor), thrombotic disorders (in | | | |
| | CC | combination with an anti-platelet agent or by local delivery through | | | |
| | CC | an intracoronary catheter), protein C deficiency, acute arterial | | | |
| | CC | cerebral or peripheral arteries or in vascular grafts. Human | | | |
| | CC | patients with genetically predisposed prothrombotic disorders may | | | |
| | CC | be treated by gene therapy (all claimed). | | | |
| SQ | XX | Sequence 1386 BP; 285 A; 417 C; 443 G; 241 T; 0 other; | | | |
| | XX | Alignment Scores: | | | |
| | Pred. No.: | 1.19e-22 | Length: | 1386 | |
| | Score: | 174.00 | Matches: | 34 | |
| | Percent Similarity: | 77.27% | Conservative: | 0 | |
| | Best Local Similarity: | 77.27% | Mismatches: | 10 | |
| | Query Match: | 88.32% | Indels: | 0 | |
| | DB: | 22 | Gaps: | 0 | |
| SEQ1-4EDITS (1-44) | XX | (1-1386) | | | |
| OY | 1 | AlaAsnSerpheLeu*****LeuArgGlnGlySerLeu***Arg***Cyste***** 20 | | | |
| Db | 127 | GCCAACTCCTTCCTGGAGGAGCTCGTCACGGAGCGCTGACGGGGAGTGCATAGAGG 186 | | | |
| Oy | 21 | IleCysAspPhe*****AlaLys***IlepheGluAspValAspaspThrLeuAlaPhe 40 | | | |
| Db | 187 | ATCTGTRGACTTCGAGGAGGCCAAGGAATTTCGAAGATGTTGATGACACTGGCTTC 246 | | | |
| Oy | 41 | TrpSerLysHis 44 | | | |
| Db | 247 | TGGTCCAAGCAC 258 | | | |
| RESULT 8 | XX | | | | |
| AAH26364 | XX | Sequence 1386 BP; 285 A; 416 C; 444 G; 241 T; 0 other; | | | |
| ID | XX | Alignment Scores: | | | |
| AC | AC | Pred. No.: | 1.19e-22 | Length: | 1386 |
| DT | DT | Score: | 174.00 | Matches: | 34 |
| | | Percent Similarity: | 77.27% | Conservative: | 0 |
| | | Best Local Similarity: | 77.27% | Mismatches: | 10 |
| DNA | DNA | encoding human protein C derivative. | | | |
| DE | DE | | | | |
| | XX | Homo sapiens. | | | |
| | OS | Synthetic. | | | |
| | XX | | | | |
| | FH | Key | | | |
| | FT | sig-peptide | | | |
| | FT | 1.126 | | | |
| | FT | /^tag= a | | | |
| | FT | 127.1183 | | | |
| | FT | /*tag= b | | | |
| | FT | note= "encodes AAB82676" | | | |
| | XX | | | | |
| | PN | WO200157193-A2. | | | |
| | XX | | | | |
| | PD | 09-AUG-2001. | | | |
| | XX | | | | |
| | PF | 19-JAN-2001; 2001WO-US00020. | | | |
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| | PR | 02-FEB-2000; 2000US-0179801. | | | |
| | XX | | | | |
| | PR | 14-MAR-2000; 2000US-0189197. | | | |
| | XX | | | | |
| | PA | (ELIL) LILLY & CO ELI. | | | |
| | XX | | | | |
| | PI | Gerlitz BE, Jones BE; | | | |
| | XX | | | | |
| | DR | WPI; 2001-490919/54. | | | |
| | DR | P-PSDB; AAB82676. | | | |
| | XX | | | | |
| | CC | The present sequence is that of DNA encoding a claimed human | | | |
| | CC | protein C derivative (see AAB82675), in which Ser at position 11 of | | | |
| | CC | the mature wild-type protein C sequence is substituted with Gly, Gln | | | |
| | CC | at position 32 with Glu, Asn at position 33 with Asp, Leu at position | | | |
| | CC | 194 with Ser, and Thr at position 254 with Ser. The invention relates | | | |
| | CC | to protein C derivatives having at least 2 amino acid substitutions, | | | |
| | CC | and to recombinant DNA molecules encoding such derivatives. These | | | |
| | CC | derivatives have increased anticoagulant activity and resistance to | | | |
| | CC | inactivation by serpins compared with wild-type human protein C but | | | |
| | CC | retain the biological activity of the wild-type protein. Recombinant | | | |
| | CC | DNA molecules encoding preferred protein C derivatives are given in | | | |
| | CC | AAH26363-66. Also claimed are a vector comprising the recombinant | | | |
| | CC | DNA, transformed host cells and a method of producing the human | | | |
| | CC | protein C derivative. The protein C derivatives are useful for | | | |
| | CC | treating coronary syndromes and disease states predisposing to | | | |
| | CC | thrombosis (e.g. myocardial infarction and unstable angina), | | | |
| | CC | vascular occlusive disorders and hypercoagulable states, sepsis (in | | | |
| | CC | combination with bactericidal permeability increasing protein or | | | |
| | CC | with tissue factor pathway inhibitor), thrombotic disorders (in | | | |
| | CC | combination with an anti-platelet agent, or by local delivery through | | | |
| | CC | an intracoronary catheter), protein C deficiency, acute arterial | | | |
| | CC | thrombotic occlusion, thromboembolism, or stenosis in coronary, | | | |
| | CC | cerebral or peripheral arteries or in vascular grafts. Human | | | |
| | CC | patients with genetically predisposed prothrombotic disorders may | | | |
| | CC | be treated by gene therapy (all claimed). | | | |
| SQ | XX | Sequence 1386 BP; 285 A; 416 C; 444 G; 241 T; 0 other; | | | |
| | XX | Alignment Scores: | | | |
| | Pred. No.: | 1.19e-22 | Length: | 1386 | |
| | Score: | 174.00 | Matches: | 34 | |
| | Percent Similarity: | 77.27% | Conservative: | 0 | |
| | Best Local Similarity: | 77.27% | Mismatches: | 10 | |

substitution in a position (P) where (P) is an amino acid with at least 25% of its side group exposed to the surface, with the proviso that the substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln, Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding (V); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V) or (VI); (5) increasing (M2) the functional in vivo half-life or the serum half-life of a parent protein C polypeptide.

The conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and diagnosis/prevention) of stroke, myocardial infarction, after venous thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence encodes zymogen protein C.

Sequence 1257 BP; 264 A; 375 C; 406 G; 212 T; 0 other;

Alignment Scores:
pred. No.: 4.51e-20 Length: 1257
Score: 160.00 Matches: 31
Percent Similarity: 75.00% Conservative: 2
Best Local Similarity: 70.45% Mismatches: 11
Query Match: 81..22% Indels: 0
DB: 24 Gaps: 0

SEQ1-4EDITS (1-44) x ABK86039 (1-1257)

QY 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***CysIle***** 20
Db 1 GCGCAACTCCCTCTCCAGGAGCTCCGTACAGCAGCTGGAGCGAGTCATAGAGGAG 60
QY 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspAspThrLeuAlaPhe 40
Db 61 ATCTGAGTCAAGCCAAATTTCCTAAATGTTGATGACACTGGCTTC 120

QY 41 TrpSerLysHis 44
Db 121 TGGTCAGAAC 132

RESULT 11
AAN60001
ID AAN60001 standard; DNA; 1260 BP.
XX
AC AAN60001;
XX
DT 25-JUL-1991 (first entry)

Sequence encoding polypeptide with human protein C activity.
Vascular disorder therapy; protein C deficiency; ss.
Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1260
FT /*tag= a
XX
PN EP191606-A.
XX

PD 20-AUG-1986.
XX
PF 06-FEB-1986; 86EP-0300823.
XX
PR 08-FEB-1985; 85US-0699967.
XX
PA (ELIL) ELI LILLY & CO.
XX
PI Bang NU, Beckmann RJ, Jaskunas SR, Lai MHT, Little SP;
PI Long GL, Santere RF;
XX
DR WPI; 1986-220077/34.
XX
PS P-PSDB; AAP60001.

Claim 1; Pages 96-97; 121pp; English.

The claimed sequence AAN60001 has "R1N-RM" attached to its 5' end

wherein: R= AAN60002 or AAN60003, and R1= AAN60004 or AAN60005; and M and N= 0 or 1; provided that when M=0, N=0; and that when R= AAN60002, R1= AAN60004; and that when R= AAN60003, R1= AAN60005.

XX Sequence 1260 BP; 265 A; 375 C; 407 G; 213 T; 0 other;

Alignment Scores:
pred. No.: 4.52e-20 Length: 1260
Score: 160.00 Matches: 31
Percent Similarity: 75.00% Conservative: 2
Best Local Similarity: 70.45% Mismatches: 11
Query Match: 81..22% Indels: 0
DB: 7 Gaps: 0

SEQ1-4EDITS (1-44) x AAN60001 (1-1260)

QY 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***CysIle***** 20
Db 1 GCGCAACTCCCTCTCCAGGAGCTCCGTACAGCAGCTGGAGCGAGTCATAGAGGAG 60
QY 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspAspThrLeuAlaPhe 40
Db 61 ATCTGAGTCAAGCCAAATTTCCTAAATGTTGATGACACTGGCTTC 120

QY 41 TrpSerLysHis 44
Db 121 TGGTCAGAAC 132

RESULT 12
AID15223
ID AID15223 standard; DNA; 1260 BP.
XX
AC AID15223;
XX
DT 01-NOV-2001 (first entry)

Human mature wild type protein C encoding DNA.
Human: protein C derivative; anticoagulation activity; thrombosis; serpin inactivation; acute coronary syndrome; myocardial infarction; vascular occlusive disorder; hypercoagulable state; angina; sepsis; disseminated intravascular coagulation; DIC; burn; transplantation; sickle cell disease; viral haemorrhagic fever; protein C deficiency; haemolytic uraemic syndrome; acute arterial thrombotic occlusion; thromboembolism; prothrombotic disorder; gene therapy; thalassaemia; ds. Homo sapiens.

OS Homo sapiens.
XX
Key Location/Qualifiers
FH CDS 1..1260
FT /*tag= a
XX
PN EP191606-A.
XX

/note= "CDS does not include start codon"
/partial

FT
FT
XX
PN
XX
PD
XX
PF
XX
PR
11-FEB-2000; 2000US-0181948.
PR
14-MAR-2000; 2000US-0189199.
XX
PA
(ELIL) LILLY & CO ELI.
XX
PT
Gerlitz BE, Grinnell BW, Jones BE;
XX
DR
WPI; 2001-514662/56.
XX
PT
P-PSDB; AAB8625.
XX
PT
protein C derivative for treating acute coronary syndromes, vascular
PT
occlusive disorders, thrombotic disorders and sepsis, comprises
XX
PS
Disclosure: Page 51-52; 59pp; English.
XX
CC
molecules encoding such derivatives. These derivatives have increased
CC
anticoagulation activity, resistance to serpin inactivation and
CC
increased sensitivity to thrombin activation compared to wild type
CC
protein C, and retains the biological activity of the wild type human
CC
protein C. Protein C derivatives are useful in the manufacture of a
CC
medicament for the treatment of acute coronary syndromes e.g. myocardial
CC
infarction and unstable angina; and disease states predisposing to
CC
disseminated intravascular coagulation (DIC), burns, transplantsations,
CC
thalassaemia, sickle cell disease, viral haemorrhagic fever and
CC
haemolytic uremic syndrome; sepsis in combination with bacterial
CC
permeability increasing protein; thrombotic disorders in combination
CC
with an anti-platelet agent; protein C deficiency; acute arterial
CC
thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral
CC
or peripheral arteries or in vascular grafts in combination with a
CC
thrombolytic agent. Nucleic acid molecules of the invention are useful
CC
for treating humans with genetically predisposed prothrombotic disorders
CC
by gene therapy. The present sequence is human mature wild type
CC
protein C encoding DNA.
XX
Sequence 1260 BP; 265 A; 375 C; 407 G; 213 T; 0 other;
Alignment Scores:
Pred. No.: 4.52e-20
Score: 160.00
Percent Similarity: 75.00%
Best Local Similarity: 70.45%
Query Match: 81.22%
DB: 22
Gaps: 0
SEQ1-4 EDITS (1-44) x AAD15223 (1-1260)
Qy 1 AlaAsnSerPheLeu*****LeuIrgGlnGlySerLeu**Arg**CysIle***** 20
Db 1 GCCAACTCCCTTCGAGGACTCCGTACAGCACCTGGAGCGGGAGTCATAGAGG 60
Qy 21 IleCysAspPhe***AlaLys***IlePheGluAspValAspAspThrLeuAlaPhe 40
Db 61 ATCTGTGACTTCGAGGAGCCAAATTCTCAAATCTGGATGACACTGGCTTC 120
Qy 41 TrpSerPheLys 41
Db 121 TGGTGTCAAGGAC 132
RESULT 13
AAH2361
ID AAH2361 standard; cDNA: 1260 BP.

XX
AC
AAH26361;
XX
DN 15-OCT-2001 (first entry)
XX
DE DNA encoding human protein C.
XX
KW Protein C; human; coronary syndrome; thrombosis; angina;
KW myocardial infarction; vascular occlusive disorder;
KW hypercoagulation; sepsis; protein C deficiency; occlusion;
KW thromboembolism; stenosis; antibacterial; immunosuppressive;
KW thrombolytic; cardiac; antianginal; anticoagulant; gene therapy;
KW ss.
XX
OS Homo sapiens.
XX
PN WO20015193-A2.
XX
PD 09-AUG-2001.
XX
PA 19-JAN-2001; 2001WO-US00020.
XX
PT 02-FEB-2000; 2000US-0179801.
XX
PR 14-MAR-2000; 2000US-0189197.
XX
PA (ELIL) LILLY & CO ELI.
XX
PT Gerlitz BE, Jones BE;
XX
DR WPI; 2001-496919/54.
P-PSDB; AAB82673.
XX
PS Disclosure: Page 57-58; 63pp; English.
XX
CC
The present sequence is that of DNA encoding human protein C
CC
mature polypeptide (see AAB82673). The invention relates to
CC
human Protein C derivatives having at least 2 amino acid
CC
substitutions, and to recombinant DNA molecules encoding such
CC
derivatives. These derivatives have increased anticoagulant
CC
activity and resistance to inactivation by serpins compared with
CC
wild-type human protein C but retain the biological activity of
CC
the wild-type protein. The amino acid substitutions are selected
CC
from H10Q, S11G, S12K, Q22E, N33D, N33F, and amino acids at
CC
positions 194, 195, 228, 249, 254, 302, or 316 of the mature protein
CC
C polypeptide substituted with Ser, Ala, Thr, His, Lys, Leu, Arg,
CC
Asn, Asp, Glu, Gly or Gln. Recombinant DNA molecules encoding
CC
preferred protein C derivatives are given in AAB2363 66. Also
CC
claimed are a vector comprising the recombinant DNA, transformed
CC
host cells and a method of producing the human protein C
CC
derivatives. The protein C derivatives are useful for treating
CC
coronary syndromes and disease states predisposing to thrombosis
CC
(e.g. myocardial infarction and unstable angina), vascular
CC
occlusive disorders and hypercoagulable states, sepsis (in
CC
combination with bactericidal permeability increasing protein or
CC
with tissue factor pathway inhibitor), thrombotic disorders (in
CC
combination with an anti-platelet agent or by local delivery through
CC
an intracoronary catheter), protein C deficiency, acute arterial
CC
thrombotic occlusion, thromboembolism, or stenosis in coronary,
CC
cerebral or peripheral arteries or in vascular grafts. Human
CC
patients with genetically predisposed prothrombotic disorders may
CC
be treated by gene therapy (all claimed).
XX
Sequence 1260 BP; 265 A; 375 C; 407 G; 213 T; 0 other;
Alignment Scores:
Pred. No.: 4.52e-20
Score: 160.00
Percent Similarity: 75.00%
Best Local Similarity: 70.45%

PT Novel conjugate useful for treating or preventing septic shock, stroke
 PT and myocardial infarction, comprises non-polypeptide group covalently
 PT attached to protein C polypeptide comprising an attachment group

XX

PS Example 4; Page 74-76; 92pp; English.

XX The invention relates to a conjugate (I) comprising at least one non-polypeptide moiety (II) (e.g. an N-glycosyl group) covalently attached to a protein C polypeptide comprising an amino acid sequence which differs from that of a parent protein C polypeptide (III) in at least one introduced and/or at least one removed amino acid residue comprising an attachment group for the non-polypeptide group (e.g. an N-glycosylation site). Also included are (1) a variant (IV) of (III) comprising a substitution in a position (P) where (P) is an amino acid with at least 25% of its side group exposed to the surface, with the proviso that the substitution is not Thr245Ser/Ala/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln/Tyr302Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln or Phe316Ser/Ala/Thr/His/Lys/Arg/Asn/Asp/Glu/Gly/Gln; (2) a nucleotide sequence (V) encoding (IV); (3) an expression vector (VI) comprising (V); (4) a host cell (VII) comprising (V) or (VI); (5) Increasing (M2) the functional in vivo half-life or the serum half-life of a parent protein C polypeptide. The conjugates, variants and protein C proteins are useful as medicaments, and in the manufacture of medicaments for the treatment (and diagnosis/prevention) of stroke, myocardial infarction, after venous thrombosis, disseminated intravascular coagulation (DIC), sepsis, septic shock, emboli e.g. pulmonary emboli, transplantation such as bone marrow transplantation, burns, pregnancy, major surgery/trauma or adult respiratory distress syndrome (ARDS). The variant protein C has an increased resistance to activation by e.g. human plasma and alpha-1 antitrypsin. The conjugates have an increased in vivo half-life, increased serum half-life, increased resistant to inhibitors, reduced renal clearance, reduced immunogenicity and/or increased bioavailability. The conjugate offers a number of advantages over the currently available APC products, including longer duration between injections, administration of less protein, and fewer side effects. Moreover, a reduced anticoagulant activity is beneficial to reduce the risk of bleeding while maintaining the antiinflammatory activity of APC (activated protein C) conjugates. This must be especially important when the conjugate has an extended plasma life. The gene for protein C is located on chromosome 2q13-q14. The present sequence encodes precursor protein C.

XX Sequence 1383 BP; 286 A; 418 C; 440 G; 239 T; 0 other;

Alignment Scores:
 Pred. No.: 5.08e-20 Length: 1383
 Score: 160.00 Matches: 31
 Percent Similarity: 75.00% Conservative: 2
 Best Local Similarity: 70.45% Mismatches: 11
 Query Match: 81.22% Indels: 0
 DB: 24 Gaps: 0

SEQ1-4-EDITS (1-44) x ABK6038 (1-1383)

Qy 1 AlaAsnSerPheLeu*****LeuArgGlnGlySarLeu**Arg**CysLeu***** 20
 Db 127 GCGAACTCCCTCTGGAGGCTCGCTCACAGCACCTGGAGGGAGTCATAGAGGAG 186
 Qy 21 IleCysAspPhe*****AlaLys**IlePheGluAspValAspAspPheLeuIlePhe 40
 Db 187 ATCTTGACTGAGGAGGCCAGGAATTTCCAAATGTTGATGACACACTGGCTTC 246
 Qy 41 TrpSerLysIle 44
 Db 247 TGGTCGAAGCAC 258

Search completed: May 23, 2003, 06:10:27
 Job time : 251 secs

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GenCore version 5.1.4_p5_4578
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Pred NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Run on: May 23, 2003, 06:03:42 ; Search time 1761 seconds
(without alignments)
404.657 Million cell updates/sec

SEQ1-4EDITS

Title: 197
Perfect score: 1
Sequence: ANSFLXXLRLqgSLRXCIXX.....XXAKKXIfedVDDTLAFWSKH 44

Scoring table: BL0SUM62

Xgapext 10.0 , Xgapext 0.5
Ygapext 6.0 , Ygapext 0.5
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=x1h
-O=/seq2_1/jsp0_spool/SCINIZER591/runat_16052003_160565_26030/app_query.fasta_1.199
-DB=EST -QMT=fastap -SUFFIX=pan.rst -MINMATCH=0.1 -LOCPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biologum62 -TRANS=human40_cdi -LIST=45
-DOALIGN=200 -THR_SCOREPCT=THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=PCL -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=SCHNIZER591@CCN1_1_1906.ernat.16052003_160565_26030 -NCPU=6 -ICPU=3
-NO_XIPXY -NO_MMAPP -LARGEQUERY -NEC_SCORES=0 -WAIT -LONGLOG -DEV -TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FRGAPOP=6 -FRGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST *

1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hcc: *
9: gb_est1: *
10: gb_est2: *
11: gb_hcc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_ph: *
21: em_gss_vrt: *
22: em_gss_fut: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rod: *

ALIGNMENTS

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------------|---------------------|
| 1 | 160 | 81.2 | 772 | 13 BT762861 | BT762861 603008383 |
| 2 | 160 | 81.2 | 876 | 9 AL531077 | AL531077 AL531077 |
| 3 | 140 | 71.1 | 338 | 9 AA880625 | AA880625 vx41e03.r |
| 4 | 140 | 71.1 | 418 | 9 A1036235 | A1036235 v183c03.r |
| 5 | 140 | 71.1 | 498 | 12 BF236313 | BF236813 6027916 |
| 6 | 140 | 71.1 | 549 | 9 AA245935 | AA245935 mx02a04.r |
| 7 | 140 | 71.1 | 546 | 9 AA771226 | AA771226 vna43b03.r |
| 8 | 140 | 71.1 | 550 | 9 AA270181 | AA270181 vjl1c06.r |
| 9 | 140 | 71.1 | 608 | 13 BI147512 | BI147512 602913922 |
| 10 | 140 | 71.1 | 651 | 12 BF532364 | BF532364 602074403 |
| 11 | 140 | 71.1 | 669 | 13 BG96923 | BG96923 602836954 |
| 12 | 140 | 71.1 | 692 | 13 BI328022 | BI328022 602979651 |
| 13 | 140 | 71.1 | 695 | 13 BI219251 | BI219251 602934387 |
| 14 | 140 | 71.1 | 699 | 13 BI554535 | BI554535 60325665 |
| 15 | 140 | 71.1 | 712 | 13 BI219338 | BI219338 602935956 |
| 16 | 140 | 71.1 | 741 | 13 B1331957 | B1331957 602984355 |
| 17 | 140 | 71.1 | 761 | 13 B1102396 | B1102396 60288063 |
| 18 | 140 | 71.1 | 767 | 12 BF531774 | BF531774 602027680 |
| 19 | 140 | 71.1 | 767 | 12 BF234618 | BF234618 602078434 |
| 20 | 140 | 71.1 | 767 | 13 BI146467 | BI146467 602913568 |
| 21 | 140 | 71.1 | 767 | 13 BI220070 | BI220070 60294985 |
| 22 | 140 | 71.1 | 772 | 13 BI247252 | BI247252 602960793 |
| 23 | 140 | 71.1 | 778 | 13 BG972357 | BG972357 602841308 |
| 24 | 140 | 71.1 | 780 | 13 BI247353 | BI247353 602960238 |
| 25 | 140 | 71.1 | 789 | 13 BI328943 | BI328943 602980592 |
| 26 | 140 | 71.1 | 790 | 9 A109831 | A109831 ue368e12.y |
| 27 | 140 | 71.1 | 801 | 9 A109786 | A1097865 ue40901.y |
| 28 | 140 | 71.1 | 816 | 12 BF531859 | BF531859 602072788 |
| 29 | 140 | 71.1 | 823 | 13 BG972355 | BG972355 602841309 |
| 30 | 140 | 71.1 | 847 | 13 BI217283 | BI217283 602933751 |
| 31 | 140 | 71.1 | 848 | 13 BI141686 | BI141686 602912947 |
| 32 | 140 | 71.1 | 854 | 13 BG971793 | BG971793 602840859 |
| 33 | 140 | 71.1 | 862 | 13 BI218479 | BI218479 602937973 |
| 34 | 140 | 71.1 | 871 | 13 BI32823 | BI32823 602985589 |
| 35 | 140 | 71.1 | 876 | 13 BI245532 | BI245532 60298427 |
| 36 | 134 | 68.0 | 771 | 9 A986009 | A986009 uct2a01.y |
| 37 | 133.5 | 67.8 | 540 | 10 AV689656 | AV689656 AV689626 |
| 38 | 133.5 | 67.8 | 608 | 10 AV689660 | AV689640 AV689640 |
| 39 | 129 | 65.5 | 532 | 10 BE664869 | BE664869 152773 MA |
| 40 | 127 | 64.5 | 617 | 9 A12869322 | A12869322 u178f03.y |
| 41 | 124 | 62.9 | 951 | 12 BF783285 | BF783285 60214018 |
| 42 | 123 | 62.4 | 515 | 13 BI342427 | BI342427 370511 MA |
| 43 | 123 | 62.4 | 541 | 10 BR015120 | BR015120 127308 MA |
| 44 | 123 | 62.4 | 565 | 12 BG84324 | BG84324 352500 MA |
| 45 | 122 | 61.9 | 419 | 10 BE032707 | BE032707 132161 MA |

RESULT 1
LOCUS BT62861
DEFINITION mRNA sequence.
ACCESSION BT62861
VERSION BT62861.1
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 772)
AUTHORS NIH-MGC http://mgc.ncbi.nlm.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: crabps-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM11471 row: e column: 21
 High quality sequence stop: 764.

FEATURES Location/qualifiers
 source
 1. .772
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5188604"
 /clone_lib="NIH_MGC_116"
 /lab_host="DH10B"
 /note="Organ: pooled colon, kidney, stomach; Vector: PCMVSPORT; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source: anonymous pool of 3 colons, age: 26 yo male, 49 yo female, 71 yo male colon, 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."

BASE COUNT 157 a 228 c 248 g 139 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1.95e-18
 Score: 150.00
 Percent Similarity: 75.00%
 Best Local Similarity: 70.45%
 Query Match: 81.22%
 DB: 13

SBQ1-4EDITS (1-44) x BI762861 (1-772)

QY 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***CysIle***** 20
 |||||||II
 Db 183 GCGCACTCTCTCTGGAGGAGTCGGCACAGCACTGGAGCAGGGAGTCATAAGGG 242

QY 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspAspThrLeuAlaPhe 40
 |||||||II
 Db 243 ATCTGTGACTTGAGGAGGCCAAGGAATTTCACAAATGTTGAGTACACTGGCTTC 302

QY 41 TrpSerIlyHis 44
 |||||||II
 Db 303 TGGTCCAGCAC 314

RESULT² AL531077

LOCUS AL531077 876 bp mRNA linear EST 13-FEB-2001
 DEFINITION AL531077 LTI_NFL001_NB04 Homo sapiens cDNA clone CS00M001Y109 5
 ACCESSION AL531077
 VERSION 1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 876)
 AUTHORS Li, W.-B., Gruber, C., Jesse, J and Polyes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Séquençage

BP 191 91006 EYRY cedex - France
 Email: secref@genoscope.cnrs.fr, Web : www.genoscope.cnrs.fr
 FEATURES Location/qualifiers
 source
 1. .876
 /organism="Homo sapiens"
 /db_xref="C50DM001Y109"
 /clone="C50DM001Y109"
 /clone_lib="LTI_NFL001_NB04"
 /sex="male"
 /tissue_type="neuroblastoma cells"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: PCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the PCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301. 610 8371 Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com>"

BASE COUNT 166 a 256 c 303 g 150 t 1 others
 ORIGIN

Alignment Scores:
 Pred. No.: 2.32e-18
 Score: 160.00
 Percent Similarity: 75.00%
 Best Local Similarity: 70.45%
 Query Match: 81.22%
 DB: 9
 Gaps: 0
 Indels: 0
 Matches: 31
 Conservative: 2
 Mismatches: 11
 Gaps: 0
 Length: 876

SBQ1-4EDITS (1-44) x AL531077 (1-876)

QY 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***CysIle***** 20
 |||||||II
 Db 180 GCGCAACTCTCTCTGGAGGAGTCGGCACAGCACTGGAGCAGGGAGTCATAAGGG 239

QY 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspAspThrLeuAlaPhe 40
 |||||||II
 Db 240 ATCTGTGACTTGAGGAGGCCAAGGAATTTCACAAATGTTGAGTACACTGGCTTC 299

RESULT 3 AA880625

LOCUS AA880625 338 bp mRNA linear EST 26-MAR-1998
 DEFINITION vx41e03_r1 Stratagene mouse vx41e03_r1 mRNA
 IMAGE:127788 5', similar to gb:X02750_cds3 PROTEIN C PRECURSOR
 (HUMAN); gb:Di0445 Mouse mRNA for protein C, complete cds (MOUSE);
 mRNA sequence.

ACCESSION AA880625
 VERSION 1
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 338)
 AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Scheibenbogen, K., Steptoe, M., Tan, F., Underwood, R., Moore, B., Theisinger, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
 TITLE The WashU-HMM Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMM Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800

http://image.llnl.gov
Plate: LLAMA46 row: P column: 03
High quality sequence stop: 498.
Location/Qualifiers
FEATURES source
1. .498
/strain="FVB/N"
/lab_xref="taxon:10090"
/clone="IMAGE:4163186"
/clone.lib="NCI_CGAP_L19"
/lab_host="BII0B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; site_1: NotI;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 107 a 140 C 147 g 104 t
ORIGIN
Alignment Scores:
Pred. No.: 4.41e-15 Length: 498
Score: 140.00 Matches: 26
Percent Similarity: 75.00% Conservative: 7
Best Local Similarity: 59.09% Mismatches: 11
Query Match: 71.07% Indels: 0
DB: 12 Gaps: 0
SEQ1-4EDITS (1-44) x BF236813 (1-498)
QY 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***CysIle***** 20
Db 218 GCCACACASCTTCGGAGAGATCGGGCAGGGCGAGGCCGAGGGAGTGTAGGGAG 277
QY 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspAspThrIleAlaPhe 40
Db 278 ATCTGTGACTTCGAGGAGGCCAGGAGATTTCACAGACACTGGCCCTC 337
QY 41 TrpSerLysHis 44
Db 338 TGGATCAAGTAC 349
RESULT 6
AA245955
LOCUS AA245955 540 bp mRNA linear EST 10-MAR-1997
DEFINITION mx2a04.r1 Soares mouse NM_ Mus musculus cDNA clone IMAGE:678990_5,
similar to gb:DI0445 Mouse mRNA for protein C, complete cds (MOUSE
); mRNA sequence.
ACCESSION AA245955
VERSION AA245955.1
KEYWORDS EST
SOURCE house mouse
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 540)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Scheibenber,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,R., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterson,R.
TITLE Unpublished (1996).
JOURNAL Contact: Marra M/Mouse EST Project
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG:18694
Seq. primer: -28n13 rev2 ER from Amersham
High quality sequence stop: 352.

BASE COUNT 112 a 149 C 166 g 113 t
ORIGIN
Alignment Scores:
Pred. No.: 4.94e-15 Length: 540
Score: 140.00 Matches: 26
Percent Similarity: 75.00% Conservative: 7
Best Local Similarity: 59.09% Mismatches: 11
Query Match: 71.07% Indels: 0
DB: 9 Gaps: 0
SEQ1-4EDITS (1-44) x AA245955 (1-540)
QY 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***CysIle***** 20
Db 186 GCCACACASCTTCGGAGAGATCGGGCAGGGCAGCCGAGGGAGTGTAGGGAG 245
QY 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspAspThrIleAlaPhe 40
Db 246 ATCTGTGACTTCGAGGAGGCCAGGAGATTTCACAGACACTGGCCCTC 305
QY 41 TrpSerLysHis 44
Db 306 TGGATCAAGTAC 317
RESULT 7
AA771326
LOCUS AA771326 546 bp mRNA linear EST 29-JAN-1998
DEFINITION vna43b03.r1 Stratagene mouse diaphragm (#93733) Mus musculus cDNA
clone IMAGE:1000973 5' similar to gb:DI0445 Mouse mRNA for protein
C, complete cds (MOUSE); mRNA sequence.
ACCESSION AA771326
VERSION AA771326.1
KEYWORDS EST
SOURCE house mouse
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 546)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Scheibenber,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,R., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterson,R.
TITLE The Marra M/Mouse EST Project
JOURNAL Unpublished (1996).
COMMENT Contact: Marra M/Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG:565189

Technologies. Note: this is a NCI_CGAP Library."

| BASE COUNT | 135 a | 180 c | 201 g | 135 t |
|------------------------|----------|---------------|-------|-------|
| ORIGIN | | | | |
| Alignment Scores: | | | | |
| Pred. No.: | 5.82e-15 | Length: | 608 | |
| Score: | 140.00 | Matches: | 26 | |
| Percent Similarity: | 75.00% | Conservative: | 7 | |
| Best Local Similarity: | 59.09% | Mismatches: | 11 | |
| Query Match: | 71.07% | Indels: | 0 | |
| DB: | 13 | Gaps: | 0 | |

SEQ1-4EDITS (1-44) x BI147512 (1-68)

| QY | 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu**Arg**CysIle***** 20 |
|----|--|
| Db | 423 GCCAACAGCTTCTGAAAGAGATGGGCCAGGCCCTGGACAGGGAGTGTGGAGGAG 482 |

QY 21 IleCysAspHe*****AlaLys***IlePheGluAspValAspAspThrLeuAlaPhe 40

| Db | 483 ATCTGAGACTGAGGAGGCCAGAGATTTCCAATATGGAGACACTGGCCTTC 542 |
|----|--|
|----|--|

QY 41 TrpSerIlyHis 44

| Db | 543 TGGATCAAGTAC 554 |
|----|----------------------|
|----|----------------------|

RESULT 10

| BF533364 | BF532364 | BF532364 | BF532364 | |
|---|--|--------------|----------|--------|
| LOCUS | 60307403F1 | 651 bp | mRNA | linear |
| DEFINITION | NCI_CGAP_Li9 | Mus musculus | cdna | clone |
| ACCESSION | IMAGE:4211329 | 5' | | |
| VERSION | 5 | | | |
| COMMENT | MRI-MGC http://mgc.ncbi.nih.gov/ | | | |
| KEYWORDS | EST | | | |
| SOURCE | house mouse | | | |
| ORGANISM | Mus musculus | | | |
| Mammalia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | | |
| REFERENCE | 1 (bases 1 to 651) | | | |
| AUTHORS | NIR-MGC http://mgc.ncbi.nih.gov/ | | | |
| TITLE | National Institutes of Health, Mammalian Gene Collection (MGC) | | | |
| JOURNAL | Unpublished (1999) | | | |
| COMMENT | Contact: Robert Strausberg, Ph.D. Email: cgbps-r@mail.nih.gov | | | |
| Tissue Procurement: Jeffrey E. Green, M.D. | | | | |
| CDNA Library Preparation: Life Technologies, Inc. | | | | |
| CDNA Library Preparation: Life Technologies, Inc. | | | | |
| DNA Sequencing by: Incyte Genomics, Inc. | | | | |
| Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://Image.Llnl.gov | | | | |
| Plate: LIAM0956 | row: 1 | column: 14 | | |
| High quality sequence stop: 659. | | | | |
| Location/Qualifiers | | | | |
| FEATURES | | | | |
| source | 1. .669 | | | |
| /clone="IMAGE:4211329" | | | | |
| /clone_lib="NCI_CGAP_Li9" | | | | |
| /lab_host="DH10B (T1 phage-resistant)" | | | | |
| /note="Organ: liver; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally; Primer: Oligo dT. | | | | |
| Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library." | | | | |

FEATURES

| source | 1. .669 |
|--|---------|
| /clone="IMAGE:4211329" | |
| /clone_lib="NCI_CGAP_Li9" | |
| /lab_host="DH10B (T1 phage-resistant)" | |
| /note="Organ: liver; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally; Primer: Oligo dT. | |
| Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library." | |

BASE COUNT

| 135 a | 180 c | 201 g | 135 t | |
|------------------------|----------|---------------|-------|--|
| ORIGIN | | | | |
| Alignment Scores: | | | | |
| Pred. No.: | 6.64e-15 | Length: | 669 | |
| Score: | 140.00 | Matches: | 26 | |
| Percent Similarity: | 75.00% | Conservative: | 7 | |
| Best Local Similarity: | 59.09% | Mismatches: | 11 | |

SEQ1-4EDITS (1-44) x BF532364 (1-61)

| QY | 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu**Arg**CysIle***** 20 |
|----|---|
| Db | 212 GCCAACAGCTTCTGGAGAGATGGCCGCCAGGCAGGCCCTGGACAGGGAGTGTGGAGGAG 271 |

QY 21 IleCysAspHe*****AlaLys***IlePheGluAspValAspAspThrLeuAlaPhe 40

| Db | 272 ATCTGAGACTGAGGAGGCCAGAGATTTCCAATATGGAGACACTGGCCTTC 331 |
|----|--|
|----|--|

QY 41 TrpSerIlyHis 44

| Db | 332 TGGATCAAGTAC 343 |
|----|----------------------|
|----|----------------------|

RESULT 11

| BG969623 | BG969623 | BG969623 | BG969623 | |
|---|--|--------------|----------|--------|
| LOCUS | 60383694F1 | 669 bp | mRNA | linear |
| DEFINITION | NCI_CGAP_Kid14 | Mus musculus | cdna | clone |
| ACCESSION | IMAGE:4971421 | 5' | | |
| VERSION | 5 | | | |
| KEYWORDS | mRNA sequence. | | | |
| VERSION | BG969623 | 1 | | |
| EST | BG969623 | 1 | | |
| SOURCE | EST | | | |
| ORGANISM | Mus musculus | | | |
| Mammalia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | | |
| REFERENCE | 1 (bases 1 to 669) | | | |
| AUTHORS | NIR-MGC http://mgc.ncbi.nih.gov/ | | | |
| TITLE | National Institutes of Health, Mammalian Gene Collection (MGC) | | | |
| JOURNAL | Unpublished (1999) | | | |
| COMMENT | Contact: Robert Strausberg, Ph.D. Email: cgbps-r@mail.nih.gov | | | |
| Tissue Procurement: Jeffrey E. Green, M.D. | | | | |
| CDNA Library Preparation: Life Technologies, Inc. | | | | |
| CDNA Library Preparation: Life Technologies, Inc. | | | | |
| DNA Sequencing by: Incyte Genomics, Inc. | | | | |
| Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://Image.Llnl.gov | | | | |
| Plate: LIAM0956 | row: 1 | column: 14 | | |
| High quality sequence stop: 659. | | | | |
| Location/Qualifiers | | | | |
| FEATURES | | | | |
| source | 1. .669 | | | |
| /clone="IMAGE:4211329" | | | | |
| /clone_lib="NCI_CGAP_Li9" | | | | |
| /lab_host="DH10B (T1 phage-resistant)" | | | | |
| /note="Organ: kidney; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally; Primer: Oligo dT. | | | | |
| Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library." | | | | |

BASE COUNT

| 152 a | 177 c | 205 g | 135 t | |
|------------------------|--------|---------------|-------|--|
| ORIGIN | | | | |
| Alignment Scores: | | | | |
| Pred. No.: | 140.00 | Length: | 669 | |
| Score: | 140.00 | Matches: | 26 | |
| Percent Similarity: | 75.00% | Conservative: | 7 | |
| Best Local Similarity: | 59.09% | Mismatches: | 11 | |

Query Match: 71.07% Index: 0
DB: 13 Gaps: 0

SEQ1-4EDITS (1-44) x BC969623 (1-669)

Qy 1 AlaasnSerpheLeu*****LeuArgGlnGlySerLeu***Arg***CysIle***** 20
Db 169 GCCAAACAGCTCCCTGAGAGATGGGCCAGGCCACCTGCAACGGAGTATGGAGGAG 228

Qy 21 IleCysAspHe*****AlaLys***IlepheGluAspValAspAspThrLeuAlphe 40
Db 229 ATCTGTGACTTCGAGGAGGCCAGGATTTCCAATGTTGGAGACACACTGGCTTC 288

Qy 41 TrpSerLysHis 44
Db 289 TGGATCAACTAC 300

RESULT 12

BI328022 81328022 692 bp mRNA linear EST 30-JUL-2001
DEFINITION 602979651FL NCI_CGAP_L1.9 Mus musculus cDNA clone IMAGE:5132533 5',
mRNA sequence.

ACCESSION BT128022
VERSION BT128022.1 GI:15012679
COMMENT EST.

KEYWORDS house mouse.
SOURCE Mus musculus.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1. (bases 1 to 692)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgbps1@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://Image.Ilnl.gov>

Plate: LLAM1325 row: e column: 14
High quality sequence stop: 689.
Locality/Qualifiers

1. .692

FEATURES source

/organism="Mus musculus"
/strain="FVB/N"
/clone="IMAGE:5132533"
/db_xref="taxon:10090"
/clone="IMAGE:5097813"
/clone_lib="NCI_CGAP_L1.9"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size: 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 153 a 184 c 217 g 138 t
ORIGIN 161 a 182 c 213 g 139 t

Alignment Scores:
Pred. No.: 7e-15 Length: 695
Score: 140.00 Matches: 26
Percent Similarity: 75.00% Conservative: 7
Best Local Similarity: 59.09% Mismatches: 11
Query Match: 71.07% Indels: 0
DB: 13 Gaps: 0

SEQ1-4EDITS (1-44) x BI218251 (1-695).

Qy 1 AlaasnSerpheLeu*****LeuArgGlnGlySerLeu***Arg***CysIle***** 20
Db 181 GCCAAACAGCTCCCTGAGAGATGGGCCAGGCCACCTGCAACGGAGTATGGAGGAG 240

Qy 21 IleCysAspHe*****AlaLys***IlepheGluAspValAspAspThrLeuAlphe 40
Db 241 ATCTGTGACTTCGAGGAGGCCAGGATTTCCAATGTTGGAGACACACTGGCTTC 300

Qy 41 TrpSerLysHis 44
Db 301 TGGATCAACTAC 312

RESULT 14

BI554535 LOCUS BI554535 699 bp mRNA linear EST 05-SEP-2001
 DEFINITION 60393565P1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5309848 5',
 mRNA sequence.
 REFERENCE 1 (bases 1 to 712)
 AUTHORS NIH-MGC http://mgc.ncbi.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 ACCESSION BI554535
 VERSION BI554535.1 GI:15441849
 KEYWORDS EST
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 AUTHORS NIH-MGC http://mgc.ncbi.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgsaps@nlm.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: IJAM11785 row: a column: 17
 High quality sequence stop: 699.
 FEATURES source
 1. 699
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:5309848"
 /clone_1lb="NCI_CGAP_Li9"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: liver; Vector: PCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size: 1.9 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 162 a 184 c 214 g 139 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 7.06e-15
 Score: 140.00
 Percent Similarity: 75.00%
 Best Local Similarity: 59.09%
 Query Match: 21.07%
 DB: 13
 Gaps: 0
 SEQ1-4 EDITS (1-44) x BI554535 (1-699)
 QY 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***CysLe***** 20
 ||||||| ||||| :||| ||||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :|||
 Db 186 GCCAACAGCTTCTGGAAAGAGATGGGCCAGCACCTGGACCGGAGCTATGGAGGAG 130
 QY 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspAspThrLeuAlaPhe 40
 ||||| ||||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :|||
 Db 131 ATCTGAGCTTCGAGGAGCTTCCAATGTTGGAGACACAGCTGGCCTTC 190
 QY 41 TrpSerLysHis 44
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 191 TGGATCAAGTAC 202
 RESULT 15
 BI219238 LOCUS BI219238 712 bp mRNA linear EST 11-JUL-2001
 DEFINITION 60393565P1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5099389 5',
 mRNA sequence.
 ACCESSION BI219238
 VERSION BI219238.1 GI:14672682
 KEYWORDS EST
 SOURCE house mouse.
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE NIH-MGC http://mgc.ncbi.nih.gov/
 AUTHORS NIH-MGC http://mgc.ncbi.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgsaps@nlm.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: IJAM1233 row: p column: 14
 High quality sequence start: 2
 High quality sequence stop: 609.
 FEATURES source
 1. 712
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:5099389"
 /clone_1lb="NCI_CGAP_Li9"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: liver; Vector: PCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size: 1.9 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 167 a 186 c 222 g 137 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 7.24e-15
 Score: 140.00
 Percent Similarity: 75.00%
 Best Local Similarity: 59.09%
 Query Match: 71.07%
 DB: 13
 Gaps: 0
 SEQ1-4 EDITS (1-44) x BI219238 (1-712)
 QY 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***CysLe***** 20
 ||||||| ||||| :||| ||||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :|||
 Db 71 GCCAACAGCTTCTGGAAAGAGATGGGCCAGCACCTGGACCGGAGCTATGGAGGAG 130
 QY 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspAspThrLeuAlaPhe 40
 ||||| ||||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :||| ||| :|||
 Db 131 ATCTGAGCTTCGAGGAGCTTCCAATGTTGGAGACACAGCTGGCCTTC 190
 QY 41 TrpSerLysHis 44
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 191 TGGATCAAGTAC 202
 Search completed: May 23, 2003, 07:19:52
 Job time : 1778 secs

GenCore version 5.1.4_p5-4578
 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model.

Run on: May 23, 2003, 06:06:29 ; Search time 54 Seconds

(Without alignments)
 249.885 Million cell updates/sec

Title: SEQ1-4EDITS

Perfect score: 197

Sequence: 1 ANSFLXXLRQQSLRXCCIXX.....XXAKX1FEdVDDTLAFWSKH 44

Scoring table: BLOSUM62

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| Ygapext | 10.0 | Ygapext | 0.5 |
| Fgapext | 6.0 | Fgapext | 7.0 |
| Del0 | 6.0 | Deletx | 7.0 |

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LIS=45 -DOCALLIGN=200 -THR_SCORE=PCF -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5 -FGAPOM=6 -FGAPEXT=7
-YGAPOM=10 -YGAPEXT=0.5 -DEL0=6 -DELEXT=7
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Database : Issued_Patents_NA,*

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6: /cgn2_6/ptodata/1/na/backfiles1.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|--------------------|
| 1 | 160 | 81.2 | 1386 | 2 US-08-756-506-3 |
| 2 | 160 | 81.2 | 1755 | 6 5225537-1 |
| 3 | 155 | 78.7 | 1387 | 6 5220178 |
| 4 | 119 | 60.4 | 1725 | 2 US-08-756-506-1 |
| 5 | 114 | 57.9 | 1554 | 1 US-08-469-486-1 |
| 6 | 114 | 57.9 | 1554 | 2 US-08-469-658-1 |
| 7 | 110 | 55.8 | 1500 | 1 US-08-487-037-4 |
| 8 | 99 | 50.3 | 1440 | 1 US-07-882-020A-3 |
| 9 | 99 | 50.3 | 1440 | 1 US-08-021-615A-3 |
| 10 | 99 | 50.3 | 1440 | 1 US-08-321-777-3 |
| 11 | 99 | 50.3 | 1440 | 1 US-08-321-777-3 |
| 12 | 99 | 50.3 | 1440 | 3 US-09-009-217-13 |

RESULT 1

US-08-756-506-3

Sequence 3, Application US/08756506

Patent No. 5505185

GENERAL INFORMATION:

APPLICANT: Garner, Ian
 APPLICANT: Cotttingham, Ian R.
 APPLICANT: Tempierley, Simon M.
 APPLICANT: Foster, Donald C.
 APPLICANT: Spreecher, Cindy A.
 APPLICANT: Prunkard, Donna E.
 TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
 TITLE OF INVENTION: ANIMALS
 NUMBER OF SEQUENCES: 25

ALIGNMENTS

| | | | | | |
|----|----|------|------|---------------------|--------------------|
| 13 | 99 | 50.3 | 1440 | 3 US-09-009-656-13 | Sequence 13, Appli |
| 14 | 99 | 50.3 | 1440 | 5 PCT-US93-0493-3 | Sequence 3, Appli |
| 15 | 99 | 50.3 | 2422 | 1 US-08-475-455-1 | Sequence 1, Appli |
| 16 | 99 | 50.3 | 2422 | 1 US-08-327-690-1 | Sequence 1, Appli |
| 17 | 99 | 50.3 | 2422 | 2 US-08-660-889-1 | Sequence 1, Appli |
| 18 | 99 | 50.3 | 2422 | 2 US-08-537-807-1 | Sequence 1, Appli |
| 19 | 99 | 50.3 | 2422 | 2 US-08-871-003-1 | Sequence 1, Appli |
| 20 | 99 | 50.3 | 2422 | 3 US-08-464-233-1 | Sequence 1, Appli |
| 21 | 99 | 50.3 | 2422 | 4 US-09-189-607-1 | Sequence 1, Appli |
| 22 | 99 | 50.3 | 2422 | 4 US-09-378-907-1 | Sequence 1, Appli |
| 23 | 99 | 50.3 | 2422 | 5 PCT-US94-05779-1 | Sequence 1, Appli |
| 24 | 99 | 50.3 | 2462 | 2 US-08-479-733A-25 | Sequence 25, Appli |
| 25 | 99 | 50.3 | 2462 | 3 US-08-479-727A-25 | Sequence 25, Appli |
| 26 | 99 | 50.3 | 2462 | 3 US-08-482-369A-25 | Sequence 25, Appli |
| 27 | 99 | 50.3 | 2462 | 5 PCT-US95-07439-25 | Sequence 25, Appli |
| 28 | 99 | 43.1 | 3284 | 1 5258288-3 | Patent No. 5258288 |
| 29 | 85 | 43.1 | 3290 | 1 US-08-435-004-1 | Sequence 1, Appli |
| 30 | 85 | 43.1 | 3290 | 1 US-08-267-307-1 | Sequence 1, Appli |
| 31 | 85 | 43.1 | 3290 | 1 US-08-651-172-67 | Sequence 67, Appli |
| 32 | 85 | 43.1 | 6811 | 3 US-08-358-928-57 | Sequence 7, Appli |
| 33 | 85 | 43.1 | 6811 | 4 US-08-952-967-7 | Sequence 7, Appli |
| 34 | 85 | 42.6 | 1869 | 3 US-07-998-72A-2 | Sequence 2, Appli |
| 35 | 84 | 42.6 | 1869 | 3 US-07-998-72A-2 | Sequence 2, Appli |
| 36 | 84 | 42.6 | 1947 | 1 US-08-463-953-2 | Sequence 2, Appli |
| 37 | 84 | 42.6 | 1947 | 1 US-08-462-361-2 | Sequence 2, Appli |
| 38 | 84 | 42.6 | 1947 | 2 US-08-479-733A-24 | Sequence 24, Appli |
| 39 | 84 | 42.6 | 1947 | 3 US-08-487-427-24 | Sequence 24, Appli |
| 40 | 84 | 42.6 | 1947 | 3 US-08-479-727A-24 | Sequence 24, Appli |
| 41 | 84 | 42.6 | 1947 | 3 US-08-488-369A-24 | Sequence 24, Appli |
| 42 | 84 | 42.6 | 1947 | 5 PCT-US92-11357-2 | Sequence 2, Appli |
| 43 | 84 | 42.6 | 1947 | 5 PCT-US95-07439-24 | Sequence 24, Appli |
| 44 | 84 | 42.6 | 1988 | 1 US-07-750-080A-15 | Sequence 15, Appli |

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOSS/MS-DOS
 SOFTWARE: Patient Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/756,506
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Sawislak, Deborah A
 REGISTRATION NUMBER: 37,438
 REFERENCE/DOCKET NUMBER: 95-28
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6672

TELEFAX: 206-442-6678 ;
 INFORMATION FOR SEQ ID NO: 3: ;
 SEQUENCE CHARACTERISTICS: ;
 LENGTH: 136 base pairs ;
 TYPE: nucleic acid ;
 STRANDEDNESS: double ;
 TOPOLOGY: linear ;
 MOLECULE TYPE: cDNA ;
 FEATURE: NAME/KEY: CDS ;
 LOCATION: 1..1380 ;
 US-08-756-506-3

Alignment Scores:
 Pred. No.: 8.3e-21 Length: 1386
 Score: 160.00 Matches: 31
 Percent Similarity: 75.00% Conservative: 2
 Best Local Similarity: 70.45% Mismatches: 11
 Query Match: 81.22% Indels: 0
 DB: 2 Gaps: 0

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 127 GCCAACTCCCTCTGAGGACCTCCGTACAGCACGCCCTGGAGCCGGAGTCATAGAGGAG 186
 QY 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspAspThrLeuIlePhe 40
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 187 ATCTTGACTCTGAGGAGCCAGGAAATTTCCAAATGGATGACACACTGGCCTTC 246
 QY 41 TRPSerLysHis 44
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 Db 247 TGGTCCAAGCAC 258

RESULT 2
 5225537-1
 ;Patent No. 5225537
 ; APPLICANT: FOSTER, DONALD
 ; TITLE OF INVENTION: METHODS FOR PRODUCING HYBRID
 ; PHOSPHOLIPID-BINDING PROTEINS
 ; NUMBER OF SEQUENCES: 14
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US07/1459, 082
 ; FILING DATE: 29-DEC-1989
 ; SEQ ID NO:1:
 ; LENGTH: 1755

Alignment Scores:
 Pred. No.: 1.1e-20 Length: 1755
 Score: 160.00 Matches: 31
 Percent Similarity: 75.00% Conservative: 2
 Best Local Similarity: 70.45% Mismatches: 11
 Query Match: 81.22% Indels: 0
 DB: 6 Gaps: 0

SEQ1-4EDITS (1..44) x 5225537-1 (1..1755)
 QY 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***CysIle***** 20
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 196 GCCAACTCCCTCTGAGGACCTCCGTACAGCACGCCCTGGAGCCGGAGTCATAGAGGAG 255
 QY 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspAspThrLeuIlePhe 40
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 256 ATCTTGACTCTGAGGAGCCAGGAAATTTCCAAATGGATGACACACTGGCCTTC 315
 QY 41 TRPSerLysHis 44
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 Db 316 TGGTCCAAGCAC 327

RESULT 3
 5270178-1

Alignment Scores:
 Pred. No.: 7.28e-20 Length: 1387
 Score: 155.00 Matches: 30
 Percent Similarity: 72.73% Conservative: 2
 Best Local Similarity: 68.18% Mismatches: 12
 Query Match: 78.68% Indels: 0
 DB: 6 Gaps: 0

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 QY 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***CysIle***** 20
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 Db 127 GCCAACTCCCTCTGAGGACCTCCGTACAGCACGCCCTGGAGCCGGAGTCATAGAGGAG 186
 QY 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspAspThrLeuIlePhe 40
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 187 ATCTTGACTCTGAGGAGCCAGGAAATTTCCAAATGGATGACACACTGGCCTTC 246
 QY 41 TRPSerLysHis 44
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 Db 247 TGGTCCAAGCAC 258

RESULT 4
 US-08-756-506-1
 Sequence 1, Application US/08756506
 Patent No. 5905185
 GENERAL INFORMATION:
 APPLICANT: Garner, Ian
 APPLICANT: Cotttingham, Ian R.
 APPLICANT: Temperley, Simon M.
 APPLICANT: Foster, Donald C.
 APPLICANT: Sprecher, Cindy A.
 APPLICANT: Prunkard, Donna E.
 TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ZymoGenetics, Inc.
 STREET: 1201 Eastlake Avenue East
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98102
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/756, 506
 FILING DATE:
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Sawislak, Deborah A.
 REGISTRATION NUMBER: 37, 438
 REFERENCE/DOCKET NUMBER: 95-28
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6672
 TELEFAX: 206-442-6672
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:

LENGTH: 11725 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: join(3520..3630, 5093..5117, 5210..5347, 5450
 ; LOCATION: .5584..8253..8395, 9269..9386, 10516..11102)
 ; US-08-756-506-1.
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 Best Local Similarity: 63.15% Mismatches: 11
 Query Match: 60.41% Indels: 0
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 Qy 21 IleCysAspHe*****AlaLys***IlePheGluAspValAspAspThrLeuAlaPhe 38
 Db 3580 ATCTGTGACTTCGACGGAGGCCAAGGAATTTCAAATGTTGGATGACACAGTA 3633
 RESULT 5
 US-08-469-486-1
 Sequence 1, Application US/08469486
 Patent No. 5739281
 GENERAL INFORMATION:
 APPLICANT: Thoegersen, Hans Christian
 APPLICANT: Hollett, Thor Las
 APPLICANT: Elzerodt, Michael
 TITLE OF INVENTION: Improved method for the refolding of
 TITLE OF INVENTION: Proteins
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/469, 486
 FILING DATE: 08/19/94
 CLASSIFICATION: 530
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/192, 060
 FILING DATE: February 4, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Paul T. Clark
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 06363/002001.
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617 542 5070
 TELEFAX: 617 542 8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1554 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 SEQ1-4EDITS (1-44) x US-08-469-486-1 (1-1554)
 Qy 1 AlbaasnSerPhelau*****LeuArgGlnGlySerLeu***Arg***CysIle***** 20
 Db 196 GGCACACTCACTCTCTGAGGAGCTGGACGAGAACCTGAGCGGAGTCCTGGAGGAG 255
 Qy 21 IleCysAspHe*****AlaLys***IlePheGluAspValAspAspThrLeuAlaPhe 40
 Db 256 GGCACACTCACTCTAGAGGAGGCCGGAGGGCTTCGAGGACGCCAGCAGGATGAATC 315
 Qy 41 TrpSerLysHis 44
 Db 316 TGGAGTAATAAC 327
 RESULT 6
 US-08-469-658-1
 Sequence 1, Application US/08469658
 Patent No. 5917018
 GENERAL INFORMATION:
 APPLICANT: Thoegersen, Hans Christian
 APPLICANT: Hollett, Thor Las
 APPLICANT: Elzerodt, Michael
 TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/469, 658
 FILING DATE: June 5, 1995
 CLASSIFICATION: 530
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/192, 060
 FILING DATE: February 4, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Paul T. Clark
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 06363/002002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617 542 5070
 TELEFAX: 617 542 8906
 TELEX: 200154

RESULT 9
US-07-882-202A-3
Sequence 3, Application US/07882202A
Patent No.: 5374617
GENERAL INFORMATION:
APPLICANT: Morrissey, James H.
APPLICANT: Comp, Philip C.
TITLE OF INVENTION: Treatment of Bleeding with Modified Tissue Factor in Combination with FVIIa
TITLE OF INVENTION: Treatment of Bleeding with Modified Tissue Factor in Combination with an Activator of Coagulation
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: Texas
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/882, 202A
FILING DATE: 13-MAY-1992
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31, 966
REFERENCE/DOCKET NUMBER: OMRF B34290
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Blood
FEATURE:
NAME/KEY: CDS
LOCATION: 36..1433
OTHER INFORMATION: /note= "Coding portion of human
; OTHER INFORMATION: factor VII cDNA"
US-07-882-202A-3

Alignment Scores:
Pred. No.: 2.78e-09
Score: 99.00
Percent Similarity: 58.54%
Best Local Similarity: 48.78%
Query Match: 50.25%
DB: 1
Gaps: 0

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Qy 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspAspThrLeuAlaPhe 40
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Oy 41 Trp 41
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Db 336 TGG 338

RESULT 10
US-08-021-615A-3
Sequence 3, Application US/08021615A
; Patent No.: 5504064
GENERAL INFORMATION:
APPLICANT: Morrissey, James H.
APPLICANT: Comp, Philip C.
TITLE OF INVENTION: Treatment of Bleeding with Modified Tissue Factor in Combination with an Activator of Coagulation
TITLE OF INVENTION: Treatment of Bleeding with Modified Tissue Factor in Combination with an Activator of
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: Texas
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021, 615A
FILING DATE: 19-FEB-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/882, 202
FILING DATE: 13-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hansen, Eugenia S.
REGISTRATION NUMBER: 31, 966
REFERENCE/DOCKET NUMBER: OMRF B34290CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Blood
FEATURE:
NAME/KEY: CDS
LOCATION: 36..1433
OTHER INFORMATION: /note= "Coding portion of human
; OTHER INFORMATION: factor VII cDNA"
US-08-021-615A-3

Alignment Scores:
Pred. No.: 2.78e-09
Score: 99.00
Percent Similarity: 58.54%
Best Local Similarity: 48.78%
Query Match: 50.25%
DB: 1
Gaps: 0

SEQ1-4EDITS (1-44) x US-08-021-615A-3 (1-1440)

Qy 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***CysIle***** 20
Db 216 GCCAACCCGGTCTGGAGGAGCTGGCGCCGGGCTCCCTGGAGGAGGTGCAAGGGAG 275

Qy 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspAspThrLeuAlaPhe 40
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Oy 41 Trp 41
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Db 276 CAGTCCTCGAGGAGGCCGGAGATCTCAAGGACGCGGAGGACGAGCTGTC 335
 Qy 41 TRP 41
 Db 336 TGG 338

RESULT 11
 US-08-321-777-3
 ; Sequence 3, Application US/08321777
 ; Patent No. 550467
 ; GENERAL INFORMATION:
 ; APPLICANT: Morrissey, James H.
 ; TITLE OF INVENTION: Treatment of Bleeding with Modified FvIIa
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Richards, Medlock & Andrews
 ; STREET: 1201 Elm Street, Suite 4500
 ; CITY: Dallas
 ; STATE: Texas
 ; COUNTRY: US
 ; ZIP: 75220-2197
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/321,777
 ; FILING DATE: 13-MAY-1992
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/882202
 ; FILING DATE: 13-MAY-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hansen, Eugenia S.
 ; REGISTRATION NUMBER: 31,966
 ; REFERENCE/DOCKET NUMBER: OMRF B34290C
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 214-939-4500
 ; TELEFAX: 214-939-4600
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1440 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; TISSUE TYPE: Blood
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 36..1433
 ; OTHER INFORMATION: /note= "Coding portion of human
 ; OTHER INFORMATION: factor VII cDNA"
 US-08-321-777-3

Alignment Scores:
 Pred. No.: 2.78e-09 Length: 1440
 Score: 99.00 Matches: 20
 Percent Similarity: 58.54% Conservative: 4
 Best Local Similarity: 48.78% Mismatches: 17
 Query Match: 50.25% Indels: 0
 DB: 1 Gaps: 0

SEQ1-4EDITS (1-44) x US-08-321-777-3 (1-1440)
 Qy 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***CysIle***** 20

Db 216 GGCACACGGGTCTTGAGGAGGAGCAGGGCTCCCTGGAGGAGGTGCAGGGAG 275
 Qy 21 IleCysAspPhe*****AlaIys***IlePheGluAspValAspAspIleLeuAlaPhe 40
 Db 276 CAGTCCTCGAGGAGGCCGGAGATCTCAAGGACGCGGAGGACGAGCTGTC 335
 Qy 41 TRP 41
 Db 336 TGG 338

RESULT 12
 US-09-009-217-13
 ; Sequence 13, Application US/09009217
 ; Patent No. 6132729
 ; GENERAL INFORMATION:
 ; APPLICANT: Thorpe, Philip E.
 ; APPLICANT: King, Steven W.
 ; APPLICANT: Gao, Boning
 ; TITLE OF INVENTION: COMBINED TISSUE FACTOR AND
 ; TITLE OF INVENTION: CHEMOTHERAPEUTIC METHODS AND COMPOSITIONS FOR COAGULATION
 ; TITLE OF INVENTION: AND TUMOR TREATMENT
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P. O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: USA
 ; ZIP: 77210
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/009,217
 ; FILING DATE: Concurrently Herewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/042,427
 ; FILING DATE: 27-MAR-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/036,205
 ; FILING DATE: 27-JAN-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/035,920
 ; FILING DATE: 22-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hibler, David W.
 ; REGISTRATION NUMBER: 41,071
 ; REFERENCE/DOCKET NUMBER: UTSD:536
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 512/418-3000
 ; TELEFAX: 512/474-7577
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1440 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 US-09-009-217-13

Alignment Scores:
 Pred. No.: 2.78e-09 Length: 1440
 Score: 99.00 Matches: 20
 Percent Similarity: 58.54% Conservative: 4
 Best Local Similarity: 48.78% Mismatches: 17
 Query Match: 50.25% Indels: 0
 DB: 3 Gaps: 0

SEQ1-4EDITS (1-44) x US-09-009-217-13 (1-1440)

RESULT 13
US-09-009-656-13
Sequence 13, Application US/09009656
Patent No. 6132730
GENERAL INFORMATION:
APPLICANT: Thorpe, Philip E.
APPLICANT: King, Steven W.
APPLICANT: Gao, Boning
TITLE OF INVENTION: COMBINED TISSUE FACTOR AND FACTOR VIIA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR COAGULATION AND TUMOR
TITLE OF INVENTION: TREATMENT
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,656
FILING DATE: Concurrently Herewith
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/042,427
FILING DATE: 27-MAR-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/036,205
FILING DATE: 27-JAN-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/035,920
FILING DATE: 22-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hbler, David W.
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: UTSD:537
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base Pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
Alignment Scores:
Pred. No.: 2.78e-09 Length: 1440
Score: 99.00 Matches: 20
Percent Similarity: 58.54% Conservative: 4
Best Local Similarity: 48.78% Mismatches: 17
Query Match: 50.25% Insets: 0
Gaps: 0
Db: 336 TGG 338

RESULT 14
PCT-US93-04493-3
Sequence 3, Application PC/TUS9304493
GENERAL INFORMATION:
APPLICANT: Comp, Philip C.
TITLE OF INVENTION: Truncated Tissue Factor and FVIIa or
FVII Activator for Blood Coagulation
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richards, Medlock & Andrews
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: Texas
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/04493
FILING DATE: 19930512
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/882202
FILING DATE: 13-MAY-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/021615
FILING DATE: 19-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Y.
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: ONRF B34290C1PC/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1440 base Pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Blood
FEATURE:
NAME/KEY: CDS
LOCATION: 36..1433
OTHER INFORMATION: /product= "Tissue Factor"
OTHER INFORMATION: /note= "Coding portion of human factor VIII cDNA"
PCT-US93-04493-3

Alignment Scores: 0.70 0.60 0.50 0.40 0.30 0.20 0.10 0.00

Score: 99.00 Matches: 20
 Percent Similarity: 58.54% Conservative: 4
 Best Local Similarity: 48.78% Mismatches: 17
 Query Match: 50.25% Indels: 0
 DB: Gaps: 0

SEQ1-4 EDITS (1-44) x PCT-US93-04493-3 (1-1440)
 QY 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***CysIle***** 20
 Db 216 GCCAAACGGGTTCCGGAGGAGCTGCGCCGGGCTCCTGGAGAGGAGGTGCAAGGGAGG 275
 QY 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspAspTrpLeuAlaPhe 40
 Db 276 CAGTGCTCCTGAGGAGGCCGGAGATCTCAAGGACGCCGGAGGAGGACGAAGCTGTC 335
 QY 41 Trp 41
 Db 336 TGG 338

RESULT 15
 US-08-475-845-1
 ; Sequence 1, Application US/08475845
 ; Patent No. 5788965
 ; GENERAL INFORMATION:
 ; APPLICANT: Berkner, Kathleen L.
 ; APPLICANT: Petersen, Lars C.
 ; APPLICANT: Hart, Charles E.
 ; APPLICANT: Hedner, Ulla
 ; APPLICANT: Bregenguard, Claus
 ; TITLE OF INVENTION: Modified Factor VII
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: One Market Plaza, Steuart Street Tower
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: U.S.A.
 ; ZIP: 94105-1492
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY DISK
 ; COMPUTER: IBM PC COMPATIBLE
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.24
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/475, 845
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/327, 690
 ; FILING DATE: 24-OCT-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/065, 725
 ; FILING DATE: 21-MAY-1993
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/662, 920
 ; FILING DATE: 28-FEB-1991
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parmelee, Steven W.
 ; REGISTRATION NUMBER: 31,990
 ; REFERENCE/DOCKET NUMBER: 1A952-8-4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 206-417-9600
 ; TELEFAX: 415-543-5043
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2422 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear

Alignment Scores:
 Pred. No.: 5.21e-09 Length: 2422
 Score: 99.00 Matches: 20
 Percent Similarity: 58.54% Conservative: 4
 Best Local Similarity: 48.78% Mismatches: 17
 Query Match: 50.25% Indels: 0
 DB: Gaps: 0

SEQ1-4 EDITS (1-44) x US-08-475-845-1 (1-2422)
 QY 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***CysIle***** 20
 Db 155 GCCAAACGGGTTCCGGAGGAGCTGCGCCGGGCTCCTGGAGAGGAGGTGCAAGGGAGG 214
 QY 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspAspTrpLeuAlaPhe 40
 Db 215 CAGTGCTCCTGAGGAGGCCGGAGATCTCAAGGACGCCGGAGGAGGACGAAGCTGTC 274
 QY 41 Trp 41
 Db 275 TGG 277

Search completed: May 23, 2003, 07:21:12
 Job time : 70 secs

MOLECULE TYPE: cDNA
 HYPOTHETICAL: N
 ANTI-SENSE: N
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 28..1420
 OTHER INFORMATION: /codon_start= 28
 OTHER INFORMATION: /product= "Factor VII"
 US-08-475-845-1

GenCore version 5.1.4_p5,4578
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Run on: May 23, 2003, 06:45:52 ; Search time 140 Seconds
(without alignments)
415.002 Million cell updates/sec

Title: SEQ1-4EDITS

Perfect score: 197

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| Ygapop | 10.0 | Ygapext | 0.5 |
| Fgapop | 6.0 | Fgapext | 7.0 |
| Delop | 6.0 | Delext | 7.0 |

Searched: 88747 seqs, 660231138 residues

Total number of hits satisfying chosen parameters: 1657494

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LOOPCL=0 -LOOPEXT=0 -INITSBITS=-START=1 -END=-1 -MATRIX=blosum62
-TRANS_humano_ccl .LISI=45 -DOCLN=200 -THR_SCORE_PCT =THR_MAX=100
-THR_MIN=15 -ALIGN=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=SCANNER591 @CGN_1_1_15 @runat_16052003_160658_26166
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-DEVTIMEOUT=20 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Database : Published_Applications_NA: *

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10: /cgn2_6/podata/2/pubpna/us10_PUBCOMB.seq:*
11: /cgn2_6/podata/2/pubpna/us10_NEW_PUB.seq:*
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13: /cgn2_6/podata/2/pubpna/us60_PUBCOMB.seq:*
14: /cgn2_6/podata/2/pubpna/us60_PUBCOMB.seq:*

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Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|--------------------------------------|
| 1 | 179 | 90.9 | 1386 | 9 US-10-182-263-11 Sequence 11, Appl |
| 2 | 179 | 90.9 | 1386 | 9 US-10-182-263-12 Sequence 12, Appl |
| 3 | 174 | 88.3 | 1386 | 9 US-10-182-263-9 Sequence 9, Appl |
| 4 | 174 | 88.3 | 1386 | 9 US-10-182-263-10 Sequence 10, Appl |

ALIGMENTS

```

RESULT 1
US-10-182-263-11
; Sequence 11, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Jones, Bryan E
; APPLICANT: Grinell, Brian W
; TITLE OF INVENTION: PROTEIN C DERIVATIVES
; FILE REFERENCE: X-13611
; CURRENT APPLICATION NUMBER: US/10/182,263
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 60/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 1
; LENGTH: 1386
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-182-263-11
Alignment Scores: 6.29e-26
Length: 1386
Matches: 35
Percent Similarity: 79.55%

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SEQ1-4EDITS (1-44) x US-10-182-263-11 (1-1386)

QY 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***CysteIle***** 20
Db 127 GCCAACRCCCTCTGGAGGAGCTCCGTCAGGGACCTGGAGCGGAGTCATAGAGGA 186

QY 21 IleCysAspPhe*****AlaLys***IlePheGluaspValaspAspThrLeuAlaPhe 40
Db 187 ATCTGTGACTTCGAGGAGGCCAAGGAATTTCGAGAGTGGATGACACTGGCCCTC 246

RESULT 2
US-10-182-263-12
Sequence 12, Application US/10182263
Publication No. US20030022354A1

GENERAL INFORMATION:

APPLICANT: Gerlitz, Bruce E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611

CURRENT APPLICATION NUMBER: US/10/182, 263

CURRENT FILING DATE: 2002-07-22

PRIOR APPLICATION NUMBER: 60/181948

PRIOR FILING DATE: 2002-02-11

PRIOR APPLICATION NUMBER: 60/189199

PRIOR FILING DATE: 2000-03-14

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.1

SEQ ID NO 12
LENGTH: 1386
TYPE: DNA
ORGANISM: Homo sapiens
US-10-182-263-12

Alignment Scores:
Pred. No.: 6,29e-26 Length: 1386
Score: 174,00 Matches: 34
Percent Similarity: 77,27% Conservative: 0
Best Local Similarity: 77,27% Mismatches: 10
Query Match: 88,32% Indels: 0
DB: 9 Gaps:

SEQ1-4EDITS (1-44) x US-10-182-263-9 (1-1386)

QY 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***CysteIle***** 20
Db 127 GCCAACRCCCTCTGGAGGAGCTCCGTCAGGGACCTGGAGCGGAGTCATAGAGGA 186

QY 21 IleCysAspPhe*****AlaLys***IlePheGluaspValaspAspThrLeuAlaPhe 40
Db 187 ATCTGTGACTTCGAGGAGGCCAAGGAATTTCGAGAGTGGATGACACTGGCCCTC 246

RESULT 4
US-10-182-263-10
Sequence 10, Application US/10182263
Publication No. US20030022354A1

GENERAL INFORMATION:

APPLICANT: Gerlitz, Bruce E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611

CURRENT APPLICATION NUMBER: US/10/182, 263

CURRENT FILING DATE: 2002-07-22

PRIOR APPLICATION NUMBER: 60/181948

PRIOR FILING DATE: 2002-02-11

PRIOR APPLICATION NUMBER: 60/189199

PRIOR FILING DATE: 2000-03-14

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.1

SEQ ID NO 10
LENGTH: 1386
TYPE: DNA
ORGANISM: Homo sapiens
US-10-182-263-10

Alignment Scores:
Pred. No.: 6,29e-25 Length: 1386
Score: 174,00 Matches: 34
Percent Similarity: 77,27% Conservative: 0
Best Local Similarity: 77,27% Mismatches: 10
Query Match: 88,32% Indels: 0
DB: 9 Gaps:

SEQ1-4EDITS (1-44) x US-10-182-263-10 (1-1386)

QY 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***CysteIle***** 20
Db 127 GCCAACRCCCTCTGGAGGAGCTCCGTCAGGGACCTGGAGCGGAGTCATAGAGGA 186

Db 247 TGGTCCAAGCAC 258

RESULT 8

US-10-182-263-8

; Sequence 8, Application US/10182263

; Publication No. US2003002234A1

; GENERAL INFORMATION:

; APPLICANT: Gerlitz, Bruce E

; APPLICANT: Jones, Bryan E

; APPLICANT: Grinnell, Brian W

; TITLE OF INVENTION: PROTEIN C DERIVATIVES

; FILE REFERENCE: X-13611

; CURRENT APPLICATION NUMBER: US/10/182,263

; CURRENT FILING DATE: 2002-07-22

; PRIOR APPLICATION NUMBER: 60/181948

; PRIOR FILING DATE: 2002-02-11

; PRIOR APPLICATION NUMBER: 60/181919

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 1386

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-182-263-8

Alignment Scores:

Pred. No.: 3.98e-22

Score: 160.00

Percent Similarity: 75.00%

Best Local Similarity: 70.45%

Query Match: 81.22%

DB: 9

SEQ1-4EDITS (1-44) x US-09-880-107-3670 (1-1843)

QY 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***CysIle***** 20

Db 127 GCCAACTCTCTCTGGAGGAGCTCCCTCACAGCAGCCTGGAGCGGGAGTCATAGGAG 186

QY 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspPheLeuAlaPhe 40

Db 187 ATCTGIGACTTCGAGGAGGCCAAGGAATTTCACAAATGTGGATGACACACTGGCCTTC 246

QY 41 TrpSerIleIle 44

Db 247 TGGTCCAAGCAC 258

RESULT 9

US-09-880-107-3670

; Sequence 3670, Application US/09880107

; Patent No. US2002019462A1

; GENERAL INFORMATION:

; APPLICANT: Mardrick, Donna

; APPLICANT: Porter, Mark

; APPLICANT: Johnson, Kory

; APPLICANT: Castle, Arthur

; APPLICANT: Elashoff, Michael

; APPLICANT: Gene Logic, Inc.

; TITLE OF INVENTION: Molecular Toxicology Modeling

; FILE REFERENCE: 44921-5038-US

; CURRENT APPLICATION NUMBER: US/09/917,800A

; CURRENT FILING DATE: 2001-07-31

; PRIOR APPLICATION NUMBER: US 60/222,040

; PRIOR FILING DATE: 2000-07-31

; PRIOR APPLICATION NUMBER: US 60/222,880

; PRIOR FILING DATE: 2000-11-02

; PRIOR APPLICATION NUMBER: US 60/290,029

; PRIOR FILING DATE: 2001-05-11

; PRIOR APPLICATION NUMBER: US 60/290,645

; PRIOR FILING DATE: 2001-05-15

; PRIOR APPLICATION NUMBER: US 60/292,336

; PRIOR FILING DATE: 2001-05-22

; PRIOR APPLICATION NUMBER: US 60/295,798

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: US 60/297,457

; PRIOR FILING DATE: 2001-06-13

; PRIOR APPLICATION NUMBER: US 60/298,884

; PRIOR FILING DATE: 2001-06-19

; PRIOR APPLICATION NUMBER: US 60/303,459

; PRIOR FILING DATE: 2001-07-09

; NUMBER OF SEQ ID NOS: 1740

; SEQ ID NO 1575

; LENGTH: 1543

; TYPE: DNA

; ORGANISM: Rattus norvegicus

; FEATURE: OTHER INFORMATION: Genbank Accession No. US2002019462A1 NM_012803

US-09-917-800A-1575

Alignment Scores:

Pred. No.: 7.25e-18

Score: 139.00

Percent Similarity: 75.00%

Best Local Similarity: 59.09%

Query Match: 70.56%

DB: 0

DB: 10 Gaps: 0

SEQ1-4EDITS (1-44) x US-09-917-800A-1575 (1-1543)

QY 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***CysIle***** 20

Db 172 GCAACAGCTCCGAGGGTGGGGCCAGGCACCTGGAGCGGAGCTATGGAGG 231

QY 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspAspThrLeuLaphe 40

Db 232 ATCTGTGACTTCGAGGGCCAGGAGATTTCAGAATGTGGAAAGACACTGGCCTT 291

QY 41 TrpSerLysIle 44

Db 292 TGGATCAAGTAC 303

RESULT 11

; Sequence 2042, Application US/09960352

; Patent No. US20020137139A1

; GENERAL INFORMATION:

; APPLICANT: Warren, Wesley C.

; APPLICANT: Tao, Nengbing

; APPLICANT: Mathialagan, Nagappan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

; FILE REFERENCE: 16511 006/37-21102981C

; CURRENT APPLICATION NUMBER: US/09/960,352

; CURRENT FILING DATE: 2001-09-24

; NUMBER OF SEQ ID NOS: 15112

; SEQ ID NO: 2042

; LENGTH: 356

; TYPE: DNA

; ORGANISM: Bos taurus

; OTHER INFORMATION: Clone ID: 09-LIB34-047-Q1-E1-C1

US-09-960-352-2042

Alignment Scores:

Pred. No.: 1.12e-16 Length: 356

Score: 129.00 Matches: 22

Percent Similarity: 72.73% Conservative: 10

Best Local Similarity: 50.00% Mismatches: 12

Query Match: 10 Indels: 0

Gaps: 0

SEQ1-4EDITS (1-44) x US-09-960-352-1089 (1-399)

QY 1 AlaAsnSerPheLeu*****LeuArgGlnGlySerLeu***Arg***CysIle***** 20

Db 187 GCCAACCTCCTTCCTGGAGGACCTGGGCCGCCAACGTTGGCGTAGCTCAGAGGAG 246

QY 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspAspThrLeuLaphe 40

Db 247 GTCCTGAGTCAGGAGCTGGGAGATTTCACAAACAGGAGACACATGGCCTC 306

QY 41 TrpSerLysIle 44

Db 307 TGGTCCAAGTAT 318

RESULT 13

; Sequence 1118, Application US/09960352

; Patent No. US20020137139A1

; GENERAL INFORMATION:

; APPLICANT: Warren, Wesley C.

; APPLICANT: Tao, Nengbing

; APPLICANT: Mathialagan, Nagappan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

; FILE REFERENCE: 16511.006/37-21102981C

; CURRENT APPLICATION NUMBER: US/09/960,352

; CURRENT FILING DATE: 2001-09-24

; NUMBER OF SEQ ID NOS: 15112

; SEQ ID NO: 1118

; LENGTH: 351

; TYPE: DNA

; ORGANISM: Bos taurus

; OTHER INFORMATION: Clone ID: 05-LIB34-061-Q1-E1-B1

US-09-960-352-1118

Alignment Scores:

Pred. No.: 1.1e-13 Length: 351

Score: 114.00 Matches: 20

Percent Similarity: 63.64% Conservative: 8

Best Local Similarity: 45.45% Mismatches: 16

Query Match: 10 Indels: 0

Gaps: 0

SEQ1-4EDITS (1-44) x US-09-960-352-1118 (1-351)

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Db 137 GCCAACCTCCTTCCTGGAGGAGCTGGAGCAGGAACCTGGCGAGACTGCTGGAGGAG 196

QY 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspAspThrLeuLaphe 40

Db 303 TGGTCCAAGTAT 314

RESULT 12

; Sequence 1089, Application US/09960352

; Patent No. US20020137139A1

; GENERAL INFORMATION:

; APPLICANT: Warren, Wesley C.

; APPLICANT: Tao, Nengbing

; APPLICANT: Mathialagan, Nagappan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

; FILE REFERENCE: 16511.006/37-21102981C

; CURRENT APPLICATION NUMBER: US/09/960,352

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Db 197 GCGTGTCACTAGAGGAGGCCGAGCTCTGGAGGACGCAGACGGATTA 256
Qy 41 TPSSRlySHis 44
Db 257 TGGAGTAATAC 268

RESULT 14
US-09-960-352-632
; Sequence 632, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEAR ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 632
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 03-LIB34-038-Q1-E1-A3
; US-09-960-352-632

Alignment Scores:
Pred. No.: 1.36e-13
Score: 114.00
Percent Similarity: 63.64%
Best Local Similarity: 45.45%
Query Match: 57.87%
DB: 10

SEQ1-4EDITS (1-44) x US-09-960-352-632 (1-414)
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Conservative: 8
Mismatches: 16
Indels: 0
Gaps: 0

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Qy 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspAspThrIleAlaPhe 40
Db 119 ATCGCAGCTACGAGGAGGTCAANGANGTGTGAGAACAGAACGATGGAGTC 178
Qy 41 Trp 41
Db 179 TGG 181

Score: 107.00
Percent Similarity: 63.41%
Best Local Similarity: 43.90%
Query Match: 54.31%
DB: 10

SEQ1-4EDITS (1-44) x US-09-867-701-9727 (1-266)
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Qy 21 IleCysAspPhe*****AlaLys***IlePheGluAspValAspAspThrIleAlaPhe 40
Db 119 ATCGCAGCTACGAGGAGGTCAANGANGTGTGAGAACAGAACGATGGAGTC 178
Qy 41 Trp 41
Db 179 TGG 181

Search completed: May 23, 2003, 09:07:35
Job time : 156 secs

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